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124366

From: Prouty, Rebecca
Sent: Thursday, June 10, 2004 2:27 PM
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Subject: Sequence Search

Art Unit 1652, Rem 3A59
Mailbox: Rem 3C70
272-0937
Serial Number: 10/019,735

CRFF

Please search and interference search SEQ NOS: 2 and 6

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/15/04
Date Completed: 6/15/04
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: 1
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 031105
WWW/Internet: _____
Other (specify): _____

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STIC SEARCH RESUL FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 14, 2004, 13:28:17 ; Search time 59 Seconds
(without alignments)
1781.486 Million cell updates/sec

Title: US-10-019-735-2

Perfect score: 2006

Sequence: 1 MKYLRRHRNPATLILAGAF.....LMMDALNPNTLGNQTOIY 372

Scoring cable: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	100.0	372	2	AAW64558 Human epl
2	2006	100.0	372	2	AAW64558 Human epl
3	2006	100.0	372	4	AAU29167 Human PRO
4	2006	100.0	372	5	ABU09716 Human PRO
5	2006	100.0	372	5	AAU11272 Human bet
6	2006	100.0	372	6	ABU58543 Human PRO
7	2006	100.0	372	6	ABU88091 Novel hum
8	2006	100.0	372	6	ABU84406 Human sec
9	2006	100.0	372	6	ABR66280 Human sec
10	2006	100.0	372	6	ABR65670 Human sec
11	2006	100.0	372	6	ABU99610 Human sec
12	2006	100.0	372	6	ABU82849 Human PRO
13	2006	100.0	372	6	ABU89970 Novel hum
14	2006	100.0	372	6	ABR68219 Human sec
15	2006	100.0	372	6	ABU96272 Novel hum
16	2006	100.0	372	6	ABU92703 Human sec
17	2006	100.0	372	6	ABO08780 Human sec
18	2006	100.0	372	6	ABO02832 Human sec
19	2006	100.0	372	6	ABR74986 Human sec
20	2006	100.0	372	6	ABR94748 Human sec
21	2006	100.0	372	6	ABU85721 Human PRO
22	2006	100.0	372	6	ABU98881 Novel hum
23	2006	100.0	372	6	ABU98096 Novel hum
24	2006	100.0	372	6	ABU91802 Novel hum
25	2006	100.0	372	6	ABU89495 Human PRO

26	2006	100.0	372	6	ABU86336 Human sec
27	2006	100.0	372	6	ABU67549 Human sec
28	2006	100.0	372	6	ABU80577 Human PRO
29	2006	100.0	372	6	ABR99495 Human sec
30	2006	100.0	372	6	ABR98885 Human sec
31	2006	100.0	372	6	ABO16408 Human sec
32	2006	100.0	372	6	ABR92308 Human sec
33	2006	100.0	372	6	ABO18949 Human sec
34	2006	100.0	372	6	ABR78370 Human sec
35	2006	100.0	372	6	ABR99464 Amino aci
36	2006	100.0	372	6	ABU85106 Novel hum
37	2006	100.0	372	6	ABO00245 Novel hum
38	2006	100.0	372	6	ABO11577 Human sec
39	2006	100.0	372	6	ABO02222 Human sec
40	2006	100.0	372	6	ABU88796 Novel hum
41	2006	100.0	372	6	ABU83491 Human sec
42	2006	100.0	372	6	ABO06292 Novel hum
43	2006	100.0	372	6	ABR59328 Human sec
44	2006	100.0	372	6	ABO09390 Human sec
45	2006	100.0	372	6	ABO19254 Novel hum

ALIGNMENTS

RESULT 1					
ID	AAW64558	standard; protein; 372 AA.			
XX	AC				
XX	AAW64558;				
XX	21-OCT-1998	(first entry)			
DE	Human epidermoid carcinoma cell line KB clone HP10328 protein.				
XX	Transmembrane domain; human; nutrition; cytokine; cell proliferation;				
KM	differentiation; immune system; stimulator; suppressor; regulator;				
KM	hematopoiesis; activin; inhibitor; chemotactic; chemokine; receptor;				
KW	hemostatic; thrombolytic; ligand; anti-inflammatory; tumour.				
XX					
OS	Homo sapiens.				
XX					
PN	90982028.A2.				
XX					
PD	22-MAY-1998.				
XX					
PF	07-NOV-1997;	97WO-JP004056.			
XX					
PR	13-NOV-1996;	96JP-00301429.			
PA	(SAGA) SAGAMI CHEM RES CENTRE.				
PA	(PROT-) PROTEGENE INC.				
XX					
PI	Kato S, Sekine S, Yamaguchi T, Kobayashi M;				
XX					
DR	WPI; 1998-297932/26.				
DR	N-PSDB; AAV49558, AAV49559.				
XX					
PT	Human protein having transmembrane domain - useful for, e.g. research and				
XX	nutrition.				
PS	Claim 1; Page 116-117; 205pp; English.				
CC	AAW64534-W64558 represent human proteins containing a transmembrane				
CC	domain. These proteins can be used for, e.g. research and nutrition, and				
CC	may have cytokine and cell proliferation/differentiation, immune				
CC	stimulating/suppressing, haematopoiesis regulating, tissue growth,				
CC	activin/inhibin, chemotactic/chemokine, haemostatic and thrombolytic,				
CC	receptor/ligand, anti-inflammatory or tumour inhibition activity				
XX					
SQ	Sequence 372 AA;				
Query Match	100.0%;	Score 2006;	DB 2;	Length 372;	

Best Local Similarity 100.0%; Pred. No. 3.9e-201;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRPNATLIIAIGAFLLLFSLIVSPPTCKVQOPPAIPBALMPTPTRPAPAP 60
DB 1 MKYLRRRPNATLIIAIGAFLLLFSLIVSPPTCKVQOPPAIPBALMPTPTRPAPAP 60
QY 61 CHANTSMVTHDPFAOPHVNQNFLLYRHCNHPFLQDVPPSKCAQPVFLLVTKSSPSNY 120
DB 61 CHANTSMVTHDPFAOPHVNQNFLLYRHCNHPFLQDVPPSKCAQPVFLLVTKSSPSNY 120
QY 121 VRELLRRTWGRERKVRGLORLFLVGTASNPHARKVNRLLLEAQTGDIQWDFHD 180
DB 121 VRELLRRTWGRERKVRGLORLFLVGTASNPHARKVNRLLLEAQTGDIQWDFHD 180
QY 181 SFENLTLKQVFLQWQETRCANASFYLVNGDDVFAHTDMVFIQDHPGRLFFVGQLIQ 240
DB 181 SFENLTLKQVFLQWQETRCANASFYLVNGDDVFAHTDMVFIQDHPGRLFFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIFPIDVFL 300
DB 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIFPIDVFL 300
QY 301 GNCLELEGLKPASHSGIRTSGVAPSOHLSSFDPCFYRDLLVHRFLPYEMLLMWDALNQ 360
DB 301 GNCLELEGLKPASHSGIRTSGVAPSOHLSSFDPCFYRDLLVHRFLPYEMLLMWDALNQ 360
QY 361 PNLTGNGTOTIY 372
DB 361 PNLTGNGTOTIY 372

RESULT 2
AAB49749
ID AAB49749 standard; protein; 372 AA.
AC AAB49749;
XX
DT 17-APR-2001 (first entry)
XX
DE Human beta 1,3-N-acetylglucosamine transferase protein G4.
XX
KW Sugar chain synthesis agent; beta 1,3-N-acetylglucosamine transferase;
KW inflammation; cancer; metastasis; human.
OS Homo sapiens.
XX
PN MO200100848-A1.
XX
PD 04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP004304.
XX
PR 29-JUN-1999; 99JP-00183437.
XX
PR 16-MAR-2000; 2000JP-00074757.
XX
PA (KYO) KYOWA HAKKO KOGYO KK.
XX
PI Sasaki K, Shiraishi N, Natsune A, Yamada Y, Nakagawa S, Sekine S;
XX
DR MPI: 2001-102895/11.
XX
DR N-PSDB; AAF29256.
XX
PT New polypeptide having beta1,3-N-acetylglucosamine transferase activity
PT for diagnosis of inflammation, cancer and cancer metastasis, development
PT of remedies, and for producing glycoconjugates.
XX
PS Claim 1; Page 151-153; 195pp; Japanese.
XX
CC This invention relates to a sugar chain synthesizing agent that contains
CC a polypeptide as the active ingredient, where the polypeptide has beta
CC 1,3-N-acetylglucosamine transferase activity. The polypeptides, DNA
CC sequences encoding them and antibodies directed against the proteins are

CC useful in the diagnosis of inflammation, cancer and its metastasis,
CC development of remedies, and for producing sugar chains and
CC glycoconjugates. Sequences AAB49748 - AAB49751 represent polypeptides of
CC the invention, having beta 1,3-N-acetylglucosamine transferase activity,
CC and polynucleotides AAF29255 - AAF29258 represent cDNA encoding them. PCR
CC primers used in the isolation and characterisation of the cDNA sequences
CC are represented by sequences AAF29259 - AAF29260

SQ Sequence 372 AA;
XX

Query Match
Best Local Similarity 100.0%; Score 2006; DB 4; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRPNATLIIAIGAFLLLFSLIVSPPTCKVQOPPAIPBALMPTPTRPAPAP 60
DB 1 MKYLRRRPNATLIIAIGAFLLLFSLIVSPPTCKVQOPPAIPBALMPTPTRPAPAP 60
QY 61 CHANTSMVTHDPFAOPHVNQNFLLYRHCNHPFLQDVPPSKCAQPVFLLVTKSSPSNY 120
DB 61 CHANTSMVTHDPFAOPHVNQNFLLYRHCNHPFLQDVPPSKCAQPVFLLVTKSSPSNY 120
QY 121 VRELLRRTWGRERKVRGLORLFLVGTASNPHARKVNRLLLEAQTGDIQWDFHD 180
DB 121 VRELLRRTWGRERKVRGLORLFLVGTASNPHARKVNRLLLEAQTGDIQWDFHD 180
QY 181 SFENLTLKQVFLQWQETRCANASFYLVNGDDVFAHTDMVFIQDHPGRLFFVGQLIQ 240
DB 181 SFENLTLKQVFLQWQETRCANASFYLVNGDDVFAHTDMVFIQDHPGRLFFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIFPIDVFL 300
DB 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIFPIDVFL 300
QY 301 GNCLELEGLKPASHSGIRTSGVAPSOHLSSFDPCFYRDLLVHRFLPYEMLLMWDALNQ 360
DB 301 GNCLELEGLKPASHSGIRTSGVAPSOHLSSFDPCFYRDLLVHRFLPYEMLLMWDALNQ 360
QY 361 PNLTGNGTOTIY 372
DB 361 PNLTGNGTOTIY 372

RESULT 3
AAU29167
ID AAU29167 standard; protein; 372 AA.
AC AAU29167;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #144.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
OS Homo sapiens.
XX
PN MO200168848-A2.
XX
PD 20-SEP-2001.
XX
PR 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
XX
PR 02-MAR-2000; 2000WO-US005841.
XX
PR 03-MAR-2000; 2000US-0187202P.
XX
PR 06-MAR-2000; 2000US-0186968P.
XX
PR 14-MAR-2000; 2000US-0189320P.
XX
PR 14-MAR-2000; 2000US-0189328P.
XX
PR 15-MAR-2000; 2000WO-US006884.

PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 11-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023128.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000MO-US034956.

PA (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2001-602746/68.
 DR N-PSDB; AAS46068.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.

PS Claim 11; Fig 288; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumor in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumor in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumor necrosis factor (TNF) alpha release from human blood.
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumors and also
 CC susceptibility to tumor development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumors, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders

XX Sequence 372 AA;

Query Match 100.0%; Score 2006; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 3.9e-201;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKTLRRHRNATLILAIQATFTLLFSILVSPPTCKVQEQPPAIPALWPTPTTPAPAP 60
 DB 1 MKTLRRHRNATLILAIQATFTLLFSILVSPPTCKVQEQPPAIPALWPTPTTPAPAP 60

OY 61 CHANTSMVTHPDEATOPQHVQNEFLLYRHCNHPFLQDVPPSKCAQVFLILVKSSESNY 120
 DB 61 CHANTSMVTHPDEATOPQHVQNEFLLYRHCNHPFLQDVPPSKCAQVFLILVKSSESNY 120
 OY 121 VRRELLRRTWGRERKVRGLQRLFLVGTASNPNHARKVNRLLLEAQTHGDILOMFHD 180
 DB 121 VRRELLRRTWGRERKVRGLQRLFLVGTASNPNHARKVNRLLLEAQTHGDILOMFHD 180
 OY 181 SFFNLTLKQVLFLOQNETRCANASPVILNGDDVFAHTDNVFFYLQDHPGRHLFVGQLIQ 240
 DB 181 SFFNLTLKQVLFLOQNETRCANASPVILNGDDVFAHTDNVFFYLQDHPGRHLFVGQLIQ 240
 OY 241 NVGPIRAFMSKYVPEVVTQNERVPPYCGGCGFLSRFTAAALRRRAHVLDIFPIDVFL 300
 DB 241 NVGPIRAFMSKYVPEVVTQNERVPPYCGGCGFLSRFTAAALRRRAHVLDIFPIDVFL 300
 OY 301 GMCLLEGLKPASHSGIRTSGVRAPSQHLSSPDCFYRDILLVHRLFLPYEMLLMDALNQ 360
 DB 301 GMCLLEGLKPASHSGIRTSGVRAPSQHLSSPDCFYRDILLVHRLFLPYEMLLMDALNQ 360
 OY 361 PNLTGNGTQIY 372
 DB 361 PNLTGNGTQIY 372

RESULT 4

ABB09716 ABB09716 standard; protein; 372 AA.

XX ABB09716;

DT 11-JUN-2002 (first entry)

DE Amino acid sequence of human polypeptide HP10328.

KW Antibody; antigen; transmembrane domain protein; HP10328.

OS Homo sapiens.

PN WO200208416-A1.

PD 31-JAN-2002.

PF 24-JUL-2001; 2001MO-JP006371.

PR 24-JUL-2000; 2000JP-00222743.

PR 24-AUG-2000; 2000JP-00254407.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Kato S, Nagata N, Fujimura N, Kobayashi M, Ito K, Ishizuka Y;

XX WPI: 2002-195877/25.

DR N-PSDB; ABL41994.

PT Antibody preparation by inoculation of an animal with a vector expressing
 PT a fusion protein of an antigen on the C-terminal side of a transmembrane
 PT domain for use as drugs, diagnostic reagents and laboratory reagents.

XX Example; Page 27-32; 45pp; Japanese.

CC The specification describes a method of antibody preparation. The method
 CC comprises inoculating an animal with a vector expressing a fusion protein
 CC having an antigen protein fused to the C-terminal side (extracellular)
 CC a transmembrane domain protein (the N-terminal side of which is
 CC intracellular), and then isolating and purifying the antibody from the
 CC animal. The antibodies can be used as drugs, vaccines, diagnostic
 CC reagents and laboratory reagents. The present sequence represents a
 CC polypeptide, designated HP10328, which was used in the course of the
 CC invention

XX Sequence 372 AA;

Query Match 100.0%; Score 2006; DB 5; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.9e-201;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRNNATLILAIAGFTLLIFSLVSPPTCKVQEQPPAIPBALAMPPTTRPADAP 60
DB 1 MKYLRRRNNATLILAIAGFTLLIFSLVSPPTCKVQEQPPAIPBALAMPPTTRPADAP 60
QY 61 CHANTSMVTHPDPATOPQHVONFLYRHCRRHFPFLQDVPKCAQPVFLLVTKSSPSNY 120
DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCRRHFPFLQDVPKCAQPVFLLVTKSSPSNY 120
QY 121 VRELLRRTWGERKVRGQLRLFLVGTASNPHKAKVNRLELEAQTGDILOMDPHD 180
DB 121 VRELLRRTWGERKVRGQLRLFLVGTASNPHKAKVNRLELEAQTGDILOMDPHD 180
QY 181 SFENLTLKQVFLQWQETRCANASFLVNGDDVFAHTDNMVFYLDHPGRHLFVGQLIQ 240
DB 181 SFENLTLKQVFLQWQETRCANASFLVNGDDVFAHTDNMVFYLDHPGRHLFVGQLIQ 240
QY 241 NVGPTRAFWSKYYVEVVTQNERYPYCGGGGFLSRTAALRRAAHVLDFPIDDVFL 300
DB 241 NVGPTRAFWSKYYVEVVTQNERYPYCGGGGFLSRTAALRRAAHVLDFPIDDVFL 300
QY 301 GNCLELEGKPAHSGIRTSQVRAVSQHLSSFDPCFYRDLILVHRFLPYEMLLMDALNQ 360
DB 301 GNCLELEGKPAHSGIRTSQVRAVSQHLSSFDPCFYRDLILVHRFLPYEMLLMDALNQ 360
QY 361 PNLTGNGOTQIY 372
DB 361 PNLTGNGOTQIY 372

RESULT 5
AAU11272
ID AAU11272 standard; protein; 372 AA.
XX
AC AAU11272;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human beta1,3-N-acetylglucosaminyltransferase (beta1,3GNT) protein.
XX
KW Human; beta1,3GNT; beta1,3-N-acetylglucosaminyltransferase; MECA-79;
KW L-selectin; L-selectin sulfotransferase-2; Crohn's disease; diabetes;
KW ulcerative colitis; inflammatory skin disorder; psoriasis; lichen planus;
KW allergic contact dermatitis; lymphoma; chronic pneumonia; LSS2-2;
KW delayed-type hypersensitivity reaction; hyperplastic thymus; antileuker;
KW antiinflammatory; antipneumatic; antidiabetic; dermatological;
KW antiallergic.
XX
OS Homo sapiens.
XX
PN WO200185177-A1.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-US015452.
XX
PR 11-MAY-2000; 2000US-00569320.
XX
PA (BURN-) BURHAM INST.
XX
PI Fukuda M, Yeh J, Hirakawa N;
XX
DR WPI; 2002-075226/10.
XX
N-PSDB; AAS16945.
XX
PT New enzyme, useful for modifying acceptor molecule, comprises an isolated
PT L-selectin sulfotransferase-2 that directs expression of L-selectin
PT ligand antigen, MECA-79 in Chinese hamster ovary cells, or intestinal
PT GlcNAc 6-sulfotransferase.

XX
PS Example 1; Fig 2; 98pp; English.
XX
CC The present invention provides a method of modifying an acceptor molecule
CC by contacting the acceptor with an isolated beta1,3-N-
CC acetylglucosaminyltransferase (beta1,3GNT) or an active fragment, where
CC beta1,3GNT directs expression of a MECA-79 antigen. The invention also
CC provides a method of treating or preventing an L-selectin-mediated
CC condition by reducing the expression or activity of a beta1,3GNT that
CC directs expression of a MECA-79 antigen. This can be done by
CC administering to the subject an oligosaccharide L-selectin antagonist
CC that inhibits binding of L-selectin to a MECA-79 antigen, for example by
CC administering antibody material that specifically binds beta1,3GNT,
CC and/or a beta1,3GNT antisense nucleic acid molecule. L-selectin
CC sulfotransferase-2 (LSS2-2) also directs MECA-79 antigen expression.
CC Alternatively, the expression or activity of LSS2-2 or its active
CC fragment can be reduced in combination with reducing the expression or
CC activity of beta1,3GNT. The method is useful for treating L-selectin
CC mediated conditions such as Crohn's disease and ulcerative colitis,
CC inflammatory disorders of the skin such as allergic contact dermatitis,
CC psoriasis and lichen planus, lymphomas, chronic pneumonia, delayed-type
CC hypersensitivity reactions, diabetes and hyperplastic thymus. This
CC sequence represents human beta1,3GNT
XX
SQ Sequence 372 AA;
XX
Query Match 100.0%; Score 2006; DB 5; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.9e-201;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRNNATLILAIAGFTLLIFSLVSPPTCKVQEQPPAIPBALAMPPTTRPADAP 60
DB 1 MKYLRRRNNATLILAIAGFTLLIFSLVSPPTCKVQEQPPAIPBALAMPPTTRPADAP 60
QY 61 CHANTSMVTHPDPATOPQHVONFLYRHCRRHFPFLQDVPKCAQPVFLLVTKSSPSNY 120
DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCRRHFPFLQDVPKCAQPVFLLVTKSSPSNY 120
QY 121 VRELLRRTWGERKVRGQLRLFLVGTASNPHKAKVNRLELEAQTGDILOMDPHD 180
DB 121 VRELLRRTWGERKVRGQLRLFLVGTASNPHKAKVNRLELEAQTGDILOMDPHD 180
QY 181 SFENLTLKQVFLQWQETRCANASFLVNGDDVFAHTDNMVFYLDHPGRHLFVGQLIQ 240
DB 181 SFENLTLKQVFLQWQETRCANASFLVNGDDVFAHTDNMVFYLDHPGRHLFVGQLIQ 240
QY 241 NVGPTRAFWSKYYVEVVTQNERYPYCGGGGFLSRTAALRRAAHVLDFPIDDVFL 300
DB 241 NVGPTRAFWSKYYVEVVTQNERYPYCGGGGFLSRTAALRRAAHVLDFPIDDVFL 300
QY 301 GNCLELEGKPAHSGIRTSQVRAVSQHLSSFDPCFYRDLILVHRFLPYEMLLMDALNQ 360
DB 301 GNCLELEGKPAHSGIRTSQVRAVSQHLSSFDPCFYRDLILVHRFLPYEMLLMDALNQ 360
QY 361 PNLTGNGOTQIY 372
DB 361 PNLTGNGOTQIY 372

RESULT 6
ABU58543
ID ABU58543 standard; protein; 372 AA.
XX
AC ABU58543;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #144.
XX
KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADBP1;
KW antibody-dependent enzyme mediated prodnug therapy.

OS	Homo sapiens.	
XX	PN	US2003027272-A1.
XX	PD	06-FEB-2003.
XX	PF	21-JUN-2002; 2002US-00176492.
XX		
PR	18-SEP-1997;	97US-0059263P.
PR	18-SEP-1997;	97US-0059266P.
PR	18-SEP-1997;	97US-0062250P.
PR	21-OCT-1997;	97US-0063486P.
PR	24-OCT-1997;	97US-0063120P.
PR	24-OCT-1997;	97US-0063121P.
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PR	28-OCT-1997;	97US-0063541P.
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PR	31-OCT-1997;	97US-0063870P.
PR	31-OCT-1997;	97US-0064103P.
PR	13-NOV-1997;	97US-0065311P.
PR	21-NOV-1997;	97US-0066120P.
PR	24-NOV-1997;	97US-0066466P.
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PR	27-MAR-1998;	98US-0079664P.
PR	27-MAR-1998;	98US-0079786P.
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PR	31-MAR-1998;	98US-0080194P.
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PR	22-APR-1998;	98US-0082797P.
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PR	12-JUN-1998;	98US-0089105P.
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PR	16-JUN-1998;	98US-0089514P.
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PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
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PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-0091478P.
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PR	26-JUN-1998;	98US-0091478P.
PR	01-JUL-1998;	98US-0091599P.
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PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
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PR 18-SEP-1998; 98US-0101014P.
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PR 01-OCT-1998; 98US-0102584P.
PR 02-OCT-1998; 98US-0102687P.
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PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 2006; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.9e-201;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRRNATLLAIGAFLLPSLIYSPPTCKVQBOBPAPALPEALAMPPTPTTAPAP 60
DB 1 MKYLRRRRNATLLAIGAFLLPSLIYSPPTCKVQBOBPAPALPEALAMPPTPTTAPAP 60
QY 61 CHANTSMVTHPDPATOPQHVONFLYRHCRAFPLLQDVPPSKCAQVFFLLVIKSSPSNY 120
DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCRAFPLLQDVPPSKCAQVFFLLVIKSSPSNY 120
QY 121 VRELLRRRWGGERKRGQLMLFLVGTASNPBARKNRLLELAQTHGDILOMDPHD 180
DB 121 VRELLRRRWGGERKRGQLMLFLVGTASNPBARKNRLLELAQTHGDILOMDPHD 180
QY 121 VRELLRRRWGGERKRGQLMLFLVGTASNPBARKNRLLELAQTHGDILOMDPHD 180
DB 121 VRELLRRRWGGERKRGQLMLFLVGTASNPBARKNRLLELAQTHGDILOMDPHD 180
QY 181 SFENLTLKOVFLQNOETRCANASFVINGDDVPAHTNMVYLLDDHPGRHLFVGOLIQ 240
DB 181 SFENLTLKOVFLQNOETRCANASFVINGDDVPAHTNMVYLLDDHPGRHLFVGOLIQ 240
QY 241 NVGPIRAFWSKTYVEVVTQNERYPYCGGGFLLSRFTAALRRAAHVLDIFPIDVFL 300
DB 241 NVGPIRAFWSKTYVEVVTQNERYPYCGGGFLLSRFTAALRRAAHVLDIFPIDVFL 300
QY 301 GNCLELKGKXPSHSGIRTSQVRAPOHLSFDPCTFYTDLLVHFLFYEMLLMMDALNQ 360
DB 301 GNCLELKGKXPSHSGIRTSQVRAPOHLSFDPCTFYTDLLVHFLFYEMLLMMDALNQ 360
QY 361 PNLTCGNOTQIY 372
DB 361 PNLTCGNOTQIY 372

DB 361 PNLTCGNOTQIY 372
RESULT 7
ID ABU88091 standard; protein; 372 AA.
XX ABU88091;
AC
XX 07-JUL-2003 (first entry)
DT
XX
DE Novel human secreted and transmembrane protein PRO1266.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
XX US2003032127-A1.
XX
XX 13-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183012.
XX
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
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XX 24-OCT-1997; 97US-0063120P.
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XX 05-MAY-1998; 98US-0084366P.

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PR 04-AUG-1998; 98US-0095282P.
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PR 06-OCT-1998; 98US-0103258P.

Query Match 100.0%; Score 2006; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.9e-201; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0;

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Db 1 MKYLRRHPNATILILAGATLLFSLVSPPTCKVQEOBPALPEALWPTPTRPAPAP 60
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Db 61 CHANTSMVTHPDATOPORVQNFLLYRCHCHPFLDVPSPKCAQVYFLLLVTKSSPSNY 120
Qy 121 VRRELLRRTWGRGKRVGLQRLPLVGTASNHNHARKKVRLLLEAQTHTGDILOWDFHD 180

DB 121 VRELLRRTWGRERKRGQLRLFLVGTASNPHEARKVNRILLEAQTHGDLIQDFHD 180
QY 181 SFFNNLTAKOVLFQWQETRCANASFTVNGDDDDVFATDDMMVFLQDHGGRHLFVGQLIQ 240
DB 181 SFFNNLTAKOVLFQWQETRCANASFTVNGDDDDVFATDDMMVFLQDHGGRHLFVGQLIQ 240
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DB 241 NVGPIRAFMSKYVPEVWTQNERYPYCGGGFLLSRFTAALRRAAVLDIFPIDVFL 300
QY 301 GNCLELEGKPAASHSIRTSQVAPSOHLSSFDPCFYRDLLVHRFLPYEMLLMDALNQ 360
DB 301 GNCLELEGKPAASHSIRTSQVAPSOHLSSFDPCFYRDLLVHRFLPYEMLLMDALNQ 360
QY 361 PNLTCGNOTOIY 372
DB 361 PNLTCGNOTOIY 372

RESULT 8
ABU84406
ID ABU84406 standard; protein; 372 AA.
AC ABU84406;
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DT 02-AUG-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) #144.
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XX Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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XX Homo sapiens.
OS
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XX US2003032112-A1.
PD 13-FEB-2003.
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XX 21-JUN-2002; 2002US-00176756.
PF
XX 18-SEP-1997; 97US-0059263P.
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 Best Local Similarity 100.0%; Pred. No. 3,9e-201;
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 DB 1 MKYLRRRNPATLILIGAFTLLFSLVSPPTCKVOEOPAPALPEALWPTPTRAPAP 60
 QY 61 CHANTSMVTHPPDPAPOHVNFLYRHGRHFPFLQDVPSPKCAQVFLILYKSSPSNY 120
 DB 61 CHANTSMVTHPPDPAPOHVNFLYRHGRHFPFLQDVPSPKCAQVFLILYKSSPSNY 120
 QY 121 VRRELLRTWGRERKVRGLQLRLFLVGTASNHEARKYNRLLEDAQTHGDTLQWDFHD 180
 DB 121 VRRELLRTWGRERKVRGLQLRLFLVGTASNHEARKYNRLLEDAQTHGDTLQWDFHD 180
 QY 181 SPFNLTLLKQVLFLOWQETRCANASFVLNGDDVFAHTDMVFFYLQDHDGRLFFVQQLQ 240
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 QY 241 NVGPIRAFWSKXYVPEVVTQNERYPYCGGGFLSRFTAALRAAHVLDIPIDVFL 300
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 QY 301 GMCLTELEGKPAHSHGIRTSGVAPSOHLSSFPDPCFYRDLILVHRELPYEMLLMDALNQ 360
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 DB 361 PNITCGNQTQIY 372
 RESULT 9
 ID ABR66280 standard; protein, 372 AA.
 XX ABR66280;
 AC 05-AUG-2003 (first entry)
 DT 05-AUG-2003 (first entry)
 XX XX
 DE Human secreted polypeptide PRO1266, SEQ ID NO:288.
 XX XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiarthritic; vulnery; gene therapy.
 OS Homo sapiens.
 XX XX
 PN US2003027278-A1.
 XX XX
 PD 06-FEB-2003.
 XX XX
 PF 21-JUN-2002; 2002US-00176987.
 XX XX
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Query Match 100.0%; Score 2006; DB 6; Length 372;
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Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 NVGPIRAFWSKYVVEVVTQNERYPYCGGGFLLSFTAAALRAHVLDIPEIDVFL 300
241 NVGPIRAFWSKYVVEVVTQNERYPYCGGGFLLSFTAAALRAHVLDIPEIDVFL 300
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301 GMLCLEBGLKPAHSIGRTSGVRAPSOHLSSFPDPCFYRDLILVHFLPYEMLLMWDLNQ 360
DB 301 GMLCLEBGLKPAHSIGRTSGVRAPSOHLSSFPDPCFYRDLILVHFLPYEMLLMWDLNQ 360
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361 PNLTGNGQIOY 372
DB 361 PNLTGNGQIOY 372

RESULT 10
ABR65670
ID ABR65670 standard; protein: 372 AA.

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AC ABR65670;
DT 05-AUG-2003 (first entry)
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XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumor necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antitherapeutic; vulnerary; gene therapy.
XX
OS Homo sapiens.

XX US2003036159-A1.
XX 20-FEB-2003.
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XX 02-JUL-2002; 2002US-00188773.
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Query Match 100.0%; Score 2006; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3,9e-201;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CHANTSMWTHDPFATOPHOVONFLIYRCHRFPLLODVPPSKAOPVFLILVIKSSPSNY 120
QY 121 VRRELLRRTWGERKRVGLQRLFLFVGTASNPHBAKRVNRLBLEAQTGDILOWDFHD 180
DB 121 VRRELLRRTWGERKRVGLQRLFLFVGTASNPHBAKRVNRLBLEAQTGDILOWDFHD 180
QY 121 SFNULTLKQV.FLOWOETRCNANASFVLANGDDVFAHTDNMFYI.QDHPGRHLEFVGOLIQ 240
DB 181 SFNULTLKQV.FLOWOETRCNANASFVLANGDDVFAHTDNMFYI.QDHPGRHLEFVGOLIQ 240
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QY 301 GMCLELBGLKPASHSGIRTSQVRAPOSHTLSFDFCFYRDULLVHR.FL.PYEM.LMWDA.LNQ 360
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DB 361 PNLTGNGOTOIY 372

RESULT 11
ABUS99610

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ID ABU99610 standard; protein; 372 AA.
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AC ABU99610;
XX
DT 09-AUG-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) #144.
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KW Human: secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003040070-A1.
XX
PD 27-FEB-2003.
XX
PF 27-JUN-2002; 2002US-00184627.
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Query Match 100.0%; Score 2006; DB 6; Length 372;
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DB 241 NVGPTRAFWSKXYVEVYVTONMERYPYCGGGGFLLSRFTAALRRAAHVLDIFPIDVFL 300
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DB 301 GMCLELEGKPAHSIGIRTSQVRAPOHLSFDFCYRDLILVHRFLFYEMLLMDALNQ 360
QY 361 PMLTCGNQTOIY 372
DB 361 PMLTCGNQTOIY 372
RESULT 12
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AC AB082849;
XX 27-JUN-2003 (first entry)
DE Human PRO polypeptide #144.
XX Human PRO polypeptide; secreted and transmembrane protein; tumour;
XX chromosome mapping; gene mapping; cytosstatic.
OS Homo sapiens.
XX
XX US2003032113-A1.
XX
XX 13-FEB-2003.
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XX 20-JUN-2002; 2002US-00176911.
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XX 18-SEP-1997; 97US-0059263P.
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Query Match

100.0%; Score 2006; DB 6; Length 372;

Best Local Similarity 100.0%; Pred. No. 3,9e-201; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CHAANSMVTHPDPAPOPOHONPILYRHGRHPILODVPSCAOQVFLILYTKSSPSNY 120

QY 121 VARELLRRTWGERKRVGLQLRLFLVGTASNPNHEAKVNRILLEAQTHGDILOQDFD 180
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121 VARELLRRTWGERKRVGLQLRLFLVGTASNPNHEAKVNRILLEAQTHGDILOQDFD 180

QY 181 SEFNILTKQVLFLOQOETCANASFTLNGDDVFAATDMVFLQDHDGRHLFVQQLIQ 240
181 SEFNILTKQVLFLOQOETCANASFTLNGDDVFAATDMVFLQDHDGRHLFVQQLIQ 240

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QY 241 NVGPIRAFASKYVPEVVTQNERYPYCGGGGFLSRFTAAALRRAAVLDIFPIDVFL 300
241 NVGPIRAFASKYVPEVVTQNERYPYCGGGGFLSRFTAAALRRAAVLDIFPIDVFL 300

Db 241 NVGPIRAFASKYVPEVVTQNERYPYCGGGGFLSRFTAAALRRAAVLDIFPIDVFL 300
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Db 361 PNITCGNQTQIY 372
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RESULT 13
ID ABU89970 standard; protein; 372 AA.
XX ABU89970;
AC ABU89970;
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DT 11-AUG-2003 (first entry)
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KM Chondrocyte differentiation; tumour necrosis factor-alpha release;
KW affinity purification.
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OS Homo sapiens.
XX
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PN US2003036147-A1.
XX
PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00187741.
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Query Match 100.0%; Score 2006; DB 6; Length 372;
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 DB 61 CHANTSMVTHPDPAPOHVNFLYRCHHFPILQDVPSPKCAQVFLLVTKSSPSNY 120

QY 121 VRRELLRRTWGRERKRGLOLRLLFLVGTASNPHARKVNRLLLEAQTGDILODFHD 180
 DB 121 VRRELLRRTWGRERKRGLOLRLLFLVGTASNPHARKVNRLLLEAQTGDILODFHD 180

QY 181 SFFNLTLKOVLFLOMETCANASFVLNGDDVFAHTDMVFFVLOHDPGRHLFVQGLIQ 240
 DB 181 SFFNLTLKOVLFLOMETCANASFVLNGDDVFAHTDMVFFVLOHDPGRHLFVQGLIQ 240

QY 241 NVGPIRAFWSKYVPVVTQNERYPYCGGGLSRFTAAALRAAHVLDIPIDVFL 300
 DB 241 NVGPIRAFWSKYVPVVTQNERYPYCGGGLSRFTAAALRAAHVLDIPIDVFL 300

QY 301 GWCLELEGKLPASHGIRTSGVAPSOHLSSFPDPCFYRDDLLVHRFLPYEMLMMDALNQ 360
 DB 301 GWCLELEGKLPASHGIRTSGVAPSOHLSSFPDPCFYRDDLLVHRFLPYEMLMMDALNQ 360

QY 361 PNLTGNOFOIY 372
 DB 361 PNLTGNOFOIY 372

RESULT 14
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 ID ABR68219
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 AC 11-AUG-2003 (first entry)
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 DT 11-AUG-2003 (first entry)
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 XX Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antirheumatic; veterinary; gene therapy.
 XX
 OS Homo sapiens.
 PN US2003027264-A1.
 XX
 XX 06-FEB-2003.
 PD
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PF 18-JUN-2002; 2002US-00174579.
XX
PR 18-SEP-1997; 97US-0059263P.
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PR 11-DEC-1997; 97US-0069335P.
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PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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DT 25-JUL-2003 (first entry)

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KW knockout; chromosome identification; tissue typing; tumour;
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Job time : 61 secs

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OM protein - protein search, using sw model

Run on: June 14, 2004, 13:45:12 ; Search time 23 Seconds

(without alignments)
834.994 Million cell updates/sec

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	421.5	21.0	326	2 US-09-055-097-6	Sequence 6, App11
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6	354	17.6	325	2 US-09-055-097-5	Sequence 5, App11
7	354	17.6	325	4 US-09-373-902-5	Sequence 5, App11
8	312	15.6	378	2 US-09-055-097-1	Sequence 1, App11
9	312	15.6	378	4 US-09-373-902-1	Sequence 1, App11
10	124	6.2	350	4 US-09-464-035A-11	Sequence 11, App1
11	124	6.2	353	4 US-09-464-035A-1	Sequence 1, App11
12	124	6.2	353	4 US-09-469-562A-1	Sequence 1, App11
13	124	6.2	363	4 US-09-849-031A-1	Sequence 1, App11
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22	95.5	4.8	412	3 US-08-586-165-9	Sequence 9, App11
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24	91	4.5	406	4 US-09-198-452A-387	Sequence 387, App
25	90.5	4.5	810	4 US-09-489-039A-9748	Sequence 9748, App
26	88.5	4.4	371	3 US-08-586-165-3	Sequence 3, App11
27	87	4.3	832	4 US-08-591-502B-64	Sequence 64, App1

28	86.5	4.3	1070	3 US-08-922-635-22	Sequence 22, App1
29	86.5	4.3	1504	4 US-09-364-206-2	Sequence 2, App11
30	85.5	4.3	2813	3 US-08-896-449A-2	Sequence 2, App11
31	85.5	4.3	2813	3 US-09-132-652-2	Sequence 2, App11
32	85	4.2	372	3 US-08-586-165-5	Sequence 5, App11
33	85	4.2	832	4 US-08-591-502B-62	Sequence 62, App11
34	84	4.2	234	4 US-09-252-991A-13670	Sequence 13670, A
35	83.5	4.2	780	4 US-09-489-039A-27989	Sequence 27989, A
36	83.5	4.2	832	4 US-08-591-502B-61	Sequence 61, App1
37	83.5	4.2	2050	2 US-08-347-594A-2	Sequence 2, App11
38	83.5	4.2	2813	4 US-09-381-261A-1	Sequence 1, App11
39	83	4.1	832	4 US-08-591-502B-63	Sequence 63, App1
40	82	4.1	328	4 US-09-489-039A-9462	Sequence 9462, App
41	82	4.1	361	4 US-09-252-991A-27989	Sequence 27989, A
42	82	4.1	510	4 US-09-540-236-2148	Sequence 2148, App
43	81	4.0	172	4 US-09-252-991A-26790	Sequence 26790, A
44	81	4.0	845	1 US-08-416-950-11	Sequence 11, App1
45	81	4.0	845	2 US-08-469-830-11	Sequence 11, App1

ALIGNMENTS

```
RESULT 1
US-09-482-180A-2
; Sequence 2, Application US/09482180A
; Patent No. 6361985
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Jasper, Stephen
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
; FILE REFERENCE: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG, ZN5SP6
; CURRENT APPLICATION NUMBER: US/09/482,180A
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/115,721
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-482-180A-2

Query Match      32.4%; Score 650; DB 4; Length 378;
Best Local Similarity 42.0%; Pred. No. 4,1e-64;
Matches 145; Conservative 43; Mismatches 141; Indels 16; Gaps 6;

22 LLLFSLVSPPTCKVQOPPAIPDEALWPTPTTPAPAPBCHANTSMVTHDFATOPQHVQ 81
41 LLLGCLPLRKAKKPAQDPFAHQPFVAPPTPRSRCP-FMHTVSSA-----SLSLPSRR 94
82 NPLLYHCHGHPPLLDQVPPSKCAQPVFLILVYKSSSNVYRRLRLRTGKREK-VRGLQ 140
95 LFTYHRCNFSIL--LEPSGCSKDPFLLAISQGHVERRAARISRWGVGMARGQ 152
141 LRLPLFVGTASNSHBAKVRRLLEBAQTHGDILODFHDSFNLTLKQVLFQWQETRC 200
153 LKLVFLGTAGSAPRA-----QLLAYSGREPDILQDFEDFNLTKELHLORVVAAC 208
201 ANASFVLNDDDDVFAHTDMNVFYLODHDFGRHLFVQQLIQNVGPIRAFMSKYVPEVVTQ 260
209 PQHFLPKKDDDDVFVHPVNLLEFLDGMDDPAQDLVGDVIRQALLPNNNTKVKYIPIPSMVR 268
261 NERYPPYCGGGGFLSLRFTAAALRAAHVLDLPIDVFLGKCLELGLKPSHSGIRTS 320
269 ATHYPPYAGGGGVNSRATVRRLOAIMDEALSLIDVFGVNCRLRLGLSPMHAAGKTF 328
321 GVAAPSQHLSSFPDPCFYRDLILVHRFLPYEMLLMMDALNPVLC 365
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Db 329 GRRP---LDPLDPCLYRGILLVHRISPLEMMWMLLVYDEGLKC 370

RESULT 2

US-09-459-133-13
; Sequence 13, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-459-133-13

Query Match 23.1%; Score 462.5; DB 4; Length 389;

Best Local Similarity 32.3%; Pred. No. 4,6e-43;
Matches 118; Conservative 52; Mismatches 136; Indels 59; Gaps 12;

QY 46 ALAMPPTPRPAPAPCHANTSM-VTHP----- 71
DB 39 ALPSPPTPNAEPPLPTNLARLGQTGPLSSAYWNQOQRLGVLPSDCTGTGVAASELL 98
QY 72 DPATQPHQVNFLLYHCHRPFL-----QDVPSKCAQP-VFLILVIKSSPSNYRRL 125
DB 99 DTLVPEQLRRFLLSAACSFPMLPAGGSPVASCSDVDVPLLAVSEBGFHAAQQA 158
QY 126 LRRTRERKVRGLQLRLFLVGT---ASNPHARKVNRLLLEAQTGDIQWPHDSF 182
DB 159 VAEWNG--SPVAG--TRLIFLIGSPVGMGP---DLSLVWESRRYGDLLMDPLDVP 210
QY 183 FVLTLKQVLFLOWQETRCANASFVINGDDVFAHTDNVFLYQDHP--GRHLFVGQILQ 240
DB 211 YKRTTKDILLTLMLSHHCDFVNFVLQVQDFAVHLPALLEHLQTLPTWASGLYGEIFT 270
QY 241 NVGPTRAFWSKYVVEVVTQNRERYPYCGGGFLLSRFTAAALRAAHVLDIFPI 300
DB 271 QAKPLKPGGPPYVPTKTFEESD-YPAVYSGGYYVIGRLAPWLQAAARVAFFPPDDVYT 329
QY 301 GMLCELEGLKPAASHGIRTSGVRAPOHLSFDPCEFYRDLVHRLFPEMLMMDALNQ 360
DB 330 GFCFRLALGLAPRAHGFLLAW---PAER--TRDPCAVAGLLVHVSPQDTIMLRHLNV 384
QY 361 PWLTC 365
DB 385 PELQC 389

RESULT 3
US-09-459-133-2
; Sequence 2, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; CURRENT FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137)...(137)
; OTHER INFORMATION: Xaa is Gly or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(397)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-459-133-2

Query Match 22.9%; Score 459.5; DB 4; Length 397;

Best Local Similarity 31.9%; Pred. No. 1e-42;
Matches 118; Conservative 55; Mismatches 150; Indels 47; Gaps 12;

QY 30 SPPTCKVQEPAPALPEALAMPPTPRPAP-----APCHA-NTS 66
DB 41 TPSPPTPANPEPTLPANLSTRLGQTLPLFAVWNQOQRLGSLPSGDSSTEGGQANGAA 100
QY 67 MWTH-PDPATQPHQVNFLLYHCHRPFLQDVP-----PSKCAQP-VFLILVIKSSP 117
DB 101 AATEIPDASYPKQLRRFLLSAACSFP--QMLPGGGGXQVSSCDVDVPLLAVXSEB 158
QY 118 SNVARELLRRTWRERKVRGLQLRLFLVGTASNPHARKVNRLLLEAQTGDIQWPHDSF 177
DB 159 GRFAERQAVRETWSAP-----GIRLFLIGSPVG-EAGPDLBVLVWESRRYSDLLMD 213
QY 178 FHSDFNLTKQVLFLOWQETRCANASFVINGDDVFAHTDNVFLYQDHP--GRHLFV 235
DB 214 FLDPVFNQTLKDLLLMLGRHCPTVSFVLRQDFAVHLPALLHLRALPPASRSLYL 273
QY 236 GQLQNVGPTRAFWSKYVVEVVTQNRERYPYCGGGFLLSRFTAAALRAAHVLDIFPI 295
DB 274 GEVFTQAMPKPKPGPPYVPSPEFEG-GYPAVYSGGYYVLAGRLAPWLQAAARVAFFPF 332
QY 296 DDVFLGMLCELEGLKPAASHGIRTSGVRAPOHLSFDPCEFYRDLVHRLFPEMLM 355
DB 333 EDVVTGICIRALGLVPPAHGFLLAW---PADRTA--DHCAFRLLVRLVPLGQASIRLM 387
QY 356 DALNQPNLTC 365
DB 388 KQLQDPRLQC 397

RESULT 4
US-09-055-097-6
; Sequence 6, Application US/09055097
; Patent No. 5955282
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible


```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerione, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1150971
;
US-09-055-097-5

```

```

Query Match          17.6%; Score 354; DB 2; Length 325;
Best Local Similarity 31.7%; Pred. No. 5,2e-31;
Matches 103; Conservative 44; Mismatches 120; Indels 58; Gaps 11;

```

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QY 72 DPATPOVQVNLIRHCRHFPFLQDV-----PPSKCA-----QPVFL 110
DB 23 DYCGLTLHLHLEINFRHF-HYPLNDDTGSGSASGLDKFAYLRVPSFTAEPVQPARLT 81
QY 111 LVIKSSPENVYRELIRRTWGERKVRGQLRLFLVGTASNPHARKVNRLLLEAQT 170
DB 82 MLTKSAVNSRRREIRRTWGEGRFSVHLRRVFLGTAESEKD-----VAMESREH 135
QY 171 GDIIQWDFHDSFFNLTLLKQVLFLOWQETRCANASFVLNGDDVFAHTDNMVFYL---QD 226
DB 136 GDIIQADFTDAYENNTLKTMLGMRWASQFNRSFYLFVDDDYVSAAKVLFKLGRRQS 195
QY 227 HDPGHNLVFGQILQVNGPIRAFWSKTYYPPEVVTQNERPPYCGGGFLLSRFTAALARRA 286
DB 196 HQP-ELLPAGHVFO-TSPLRHKSFKWYVSLSEYPPDRWPVYTAGAFILSQALRQLYAA 253
QY 287 AHVLDIFPIDVFLQMCLEGLKPAASHGIRTSQVRAPSOHLSSF-----DPCFYR 338
DB 254 SVHLPLFRFDVYLGIV-----ALKAGISL-----QHCDDFRHRPRAYKGPDSYS 298
QY 339 DLLLVHRR-LPEYMLLMMDALNQPN 362
DB 299 SVIASHERFGDPPEMTVRVWNECRSAN 323

```

```

RESULT 7
US-09-373-902-5
; Sequence 5, Application US/09373902
; Patent No. 6649737
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Guegler, Karl J.
; Corley, Neil C.
; Shah, Purvi
; Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```

```

;
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/373,902
; FILING DATE: 12-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerione, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1150971
;
US-09-373-902-5

```

```

Query Match          17.6%; Score 354; DB 4; Length 325;
Best Local Similarity 31.7%; Pred. No. 5,2e-31;
Matches 103; Conservative 44; Mismatches 120; Indels 58; Gaps 11;

```

```

QY 72 DPATPOVQVNLIRHCRHFPFLQDV-----PPSKCA-----QPVFL 110
DB 23 DYCGLTLHLHLEINFRHF-HYPLNDDTGSGSASGLDKFAYLRVPSFTAEPVQPARLT 81
QY 111 LVIKSSPENVYRELIRRTWGERKVRGQLRLFLVGTASNPHARKVNRLLLEAQT 170
DB 82 MLTKSAVNSRRREIRRTWGEGRFSVHLRRVFLGTAESEKD-----VAMESREH 135
QY 171 GDIIQWDFHDSFFNLTLLKQVLFLOWQETRCANASFVLNGDDVFAHTDNMVFYL---QD 226
DB 136 GDIIQADFTDAYENNTLKTMLGMRWASQFNRSFYLFVDDDYVSAAKVLFKLGRRQS 195
QY 227 HDPGHNLVFGQILQVNGPIRAFWSKTYYPPEVVTQNERPPYCGGGFLLSRFTAALARRA 286
DB 196 HQP-ELLPAGHVFO-TSPLRHKSFKWYVSLSEYPPDRWPVYTAGAFILSQALRQLYAA 253
QY 287 AHVLDIFPIDVFLQMCLEGLKPAASHGIRTSQVRAPSOHLSSF-----DPCFYR 338
DB 254 SVHLPLFRFDVYLGIV-----ALKAGISL-----QHCDDFRHRPRAYKGPDSYS 298
QY 339 DLLLVHRR-LPEYMLLMMDALNQPN 362
DB 299 SVIASHERFGDPPEMTVRVWNECRSAN 323

```

```

RESULT 8
US-09-055-097-1
; Sequence 1, Application US/0905097
; Patent No. 5955282
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Guegler, Karl J.
; Corley, Neil C.
; APPLICANT: Corley, Neil C.

```

```

; APPLICANT: Shah, Puryl
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: DUODNOT02
; CLONE: 1705085
; US-09-055-097-1

```

```

Query Match          15.6%; Score 312; DB 2; Length 378;
Best Local Similarity 29.9%; Pred. No. 3,4e-26;
Matches 84; Conservative 43; Mismatches 116; Indels 38; Gaps 6;

QY 106 PVLILLIVIKSSPNSYVRELLRRTWGRERKVRGLQLRLFLVGTASNPHEA-RKVRRLLE 164
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 70 PPLLLIVCTAPENLQNRNIRASWGLREARGLRVOTFLGLGPNAGHPVWGSQSDLA 129
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 LEAQTGDIQWDFHDSFNNLTAKQVLFQMOETRCANASFLVNGDDVFAHTDNMFYL 224
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 130 SESAAQGDILQAAFODSYRNLTILKTLISGLNMAEKHCPMARYVLTDDVYVNPVELSEL 189
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 225 -----QHDHGRH-----LFGQLIQNVGPIFAFMSKYVPEV 257
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 190 VLGRMGWQMERSTEQREABEGGOVLHSEVPLYLGLVHWRVNPSTRPGGRHRVSEE 249
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 258 VTQNE--RYPPYCGGGGFLSFTAAALRRAAHVLDIFPIDVFLGMCLEGLKPAHS 315
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 250 QWPHTWGPPRPVYASGVYLSASAVOILIKVASRAFLPLEDFVGVASRRGLAP---- 305
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 316 GIRTSGVRAPSGHLSFDPGCFYRDLLV-HRFLPYEMLWM 355
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 306 ---TCCVKLAGATHYPLDRCCYCKFLTSHRLDPWMOEAM 343
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

; Corley, Neil C.
; Shah, Puryl
; Patterson, Chandra
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/373,902
; FILING DATE: 12-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0490 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: DUODNOT02
; CLONE: 1705085
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-373-902-1

```

```

Query Match          15.6%; Score 312; DB 4; Length 378;
Best Local Similarity 29.9%; Pred. No. 3,4e-26;
Matches 84; Conservative 43; Mismatches 116; Indels 38; Gaps 6;

QY 106 PVLILLIVIKSSPNSYVRELLRRTWGRERKVRGLQLRLFLVGTASNPHEA-RKVRRLLE 164
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 70 PPLLLIVCTAPENLQNRNIRASWGLREARGLRVOTFLGLGPNAGHPVWGSQSDLA 129
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 LEAQTGDIQWDFHDSFNNLTAKQVLFQMOETRCANASFLVNGDDVFAHTDNMFYL 224
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 130 SESAAQGDILQAAFODSYRNLTILKTLISGLNMAEKHCPMARYVLTDDVYVNPVELSEL 189
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 225 -----QHDHGRH-----LFGQLIQNVGPIFAFMSKYVPEV 257
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 190 VLGRMGWQMERSTEQREABEGGOVLHSEVPLYLGLVHWRVNPSTRPGGRHRVSEE 249
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 258 VTQNE--RYPPYCGGGGFLSFTAAALRRAAHVLDIFPIDVFLGMCLEGLKPAHS 315
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 250 QWPHTWGPPRPVYASGVYLSASAVOILIKVASRAFLPLEDFVGVASRRGLAP---- 305
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 316 GIRTSGVRAPSGHLSFDPGCFYRDLLV-HRFLPYEMLWM 355
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 306 ---TCCVKLAGATHYPLDRCCYCKFLTSHRLDPWMOEAM 343
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

```

RESULT 10
US-09-464-035A-11
; Sequence 11, Application US/09464035A
; Patent No. 6492152
; GENERAL INFORMATION:
; Guegler, Karl J.

```

```

: APPLICANT: Canfield et al.
: TITLE OF INVENTION: Core 1 3-Galactosyl Transferases & Methods of Use
: FILE REFERENCE: 5820,514
: CURRENT APPLICATION NUMBER: US/09/464,035A
: CURRENT FILING DATE: 1999-12-15
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: WordPerfect 8.0 *Software*
: SEQ ID NO 11
: LENGTH: 350
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-464-035A-11

```

Query Match	6.2%	Score 124	DB 4	Length 350
Best Local Similarity	20.1%	Pred. No. 3.6e-05		
Matches 50; Conservative	43;	Mismatches 74;	Indels 82;	Gaps 10

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Qy      105 QPVELLTLVIKSSPSVYVR-ELRLRTWGRKRKVGLRLFLVLGTASNPHEARKNRL 163
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Db      72 QVRLLCWMTGPDLKKKAHVKTW-----AQRCKNL 106
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164 ELAQTHGD-----LLQWDFHDSFELTLTKQVLFLQWQRCRANSFVLNDDDDVFAHTD 218
 107 FMSSENRKPPAVGILTKRGKQDLTKTILAFQY--HEHYLEDADWFLKRADDDTIYILD 164

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QY      219 NMVFYLDHDPGRHLEFVGGLIQNVGIRAFMSKYYVEVVTQNERPPY-----CGGGG 272
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Db      200 YLKR--EALKR--FVDAKTKDCTHSSSIDELALGRCHIEINNVAGSDRTIGETP    253
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QY	321	GVRAPSQHL	329
Db	254	HPFVREHHL	262

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RESULT 11
US-09-464-035A-1
; Sequence 1, Application US/09464035A
; Patent No. 6492152
; GENERAL INFORMATION:
; APPLICANT: Canfield et al.
; TITLE OF INVENTION: Core 1 3-Galactosyl Transferases & Methods of Use
; FILE REFERENCE: 5820.534
; CURRENT APPLICATION NUMBER: US/09/464,035A
; CURRENT FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: wordperfect 8.0 *Software*
; SEQ ID NO 1
; LENGTH: 363
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-464-035A-1

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Best Local Similarity	20.1%	Pred. No. 3.9e-05;		
Matches 50; Conservative	43;	Mismatches 74;	Indels 82;	Gaps 10;

QY 105 QPEVLLLVIKSPSNYYRR-ELLRTWGERKVRGLQLRLFLVGTASNPHEARKVNRLL 163
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DB 85 QRRLICWMVTSPQNLEKAKAHKATW-----AQRCKNVL 119

QY 164 ELEAQTGDI-----ILQADFHDSFENLLTKQVLFQMQETRCMASFLVNGDDVFAHTD 218

Db 120 FMSSEKNDFPVAVGLKTKRGRQQLYKTIKAFQYV--HEHYTEDADWFLKADDDTYVILL 177

QY 219 NMVFYLODHPGRHLEFVGQLIQNVGPILAFWMSKTYVEPVVTQNERIPY-----CGGGG 272Z

Db 178 NLRWLSTKYDDPEPPIYFGR-----RFKPYVKQGMSSGAG 212Z

QY 273 FLISRFIAALRPAHVLDIF-----PIDDVFLGMCLEBGLKEASHS---GIRTS 320

Db	213	YVLSK---	EALKR---	PVDAFKTDKCTHTSSIEDIALGRCEIINNVNAGDSRDTIGKETF	266
Qy	321	GVAPFSQL	329		
Db	267	HPFVPEHHL	275		

RESULT 12
US-09-849-562A-1
; Sequence 1, Application US/09849562A

GENERAL INFORMATION:
APPLICANT: Cummings, Richard D.
APPLICANT: McVeer, Rodger P.

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1 FILE REFERENCE: 5820 594
2
3 CURRENT APPLICATION NUMBER: US/09/849,562A
4
5 CURRENT FILING DATE: 2001-05-04
6

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; PRIOR FILING DATE: 1999-06-15
;
; NUMBER OF SEQ ID NOS: 40
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; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-562A-1

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Query Match	6.2%;	Score 124;	DB 4;	length 363;
Best Local Similarity	20.1%;	Pred. No. 3.9e-05;		
Matches 50;	Conservative 43;	Mismatches 74;	Indels 82;	Gaps 10;

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Db      120 FMSSEENKDFPAVGLTKKEGRDQLYWKTIKAFQYV--HENHLEADADWFLKADDTTYVILD 177

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Dy 219 NMVFYLDHDEGRHLFEVGLIQNVGPIRAFWSKYYVEEVTQNERIPPY-----CGGGG 27
| : | : || : : | : |
Db 178 NLRMLISKYDDEEPITFGR-----RPFKPVVKQGYSMGAG 21

Qy 273 FLSRFTAAALRRAAHVLDIF-----PIDDVFLCMCLTELEGKAKASHS---GIRIS 32
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Db 213 YVLSK--EALKR--FVDAFTDKCTHSSIEDLALGRCMELNNVBAQDSRDTIGKEFP 26

QY	321	GVRAPSQHL	329
Db	267	HPFVPEHHL	275

RESULT 13

; Sequence 1, Application US/09849031A
; Patent No. 6569998
; GENERAL INFORMATION:
; ADDITIONAL Comment: Richard D

APPLICANT McEwer, Rodger P.
TITLE OF INVENTION: synthetic glycosulfopeptides and methods of synthesis thereof
FILE REFERENCE: 5820 593
PUBLICATION NUMBER: US/09/849 031A

! CURRENT FILING DATE: 2001-05-04
! PRIOR APPLICATION NUMBER: 09/334,013
! PRIOR FILING DATE: 1999-06-15
! PRIORITY OF PTO TO VOC: 40

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 363
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ORGANISM: Homo sapiens

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 13:47:43 ; Search time 48 Seconds
(without alignments)
2183.377 Million cell updates/sec

Title: US-10-019-735-2

Perfect score: 2006

Sequence: 1 MKYLRRRRNATLILAIAGAF.....LMMDALNQPLTLCGNTQY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2006	100.0	372	10	US-09-284-320-25 Sequence 25, Appl
2	2006	100.0	372	12	US-10-206-915-288 Sequence 288, App
3	2006	100.0	372	12	US-10-199-670-288 Sequence 288, App
4	2006	100.0	372	12	US-10-201-858-288 Sequence 288, App
5	2006	100.0	372	12	US-10-205-890-288 Sequence 288, App
6	2006	100.0	372	12	US-10-208-024-288 Sequence 288, App
7	2006	100.0	372	12	US-10-201-853-288 Sequence 288, App
8	2006	100.0	372	12	US-10-174-581-288 Sequence 288, App
9	2006	100.0	372	12	US-10-176-483-288 Sequence 288, App
10	2006	100.0	372	12	US-10-176-749-288 Sequence 288, App
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19	2006	100.0	372	12	US-10-194-363-288 Sequence 288, App
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22	2006	100.0	372	12	US-10-194-484-288 Sequence 288, App
23	2006	100.0	372	12	US-10-195-884-288 Sequence 288, App
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25	2006	100.0	372	12	US-10-196-744-288 Sequence 288, App
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45	2006	100.0	372	12	US-10-208-027-288 Sequence 288, App

ALIGNMENTS

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; Sequence 25, Application US/09284320	
; Publication No. US20030092175A1	
; GENERAL INFORMATION:	
; APPLICANT: Kato, Seishi et al.	
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs	
; FILE OF INVENTION: ENCODING THESE PROTEINS	
; FILE REFERENCE: GIN-6705C9US	
; CURRENT APPLICATION NUMBER: US/09/284,320	
; CURRENT FILING DATE: 1999-06-21	
; PRIOR APPLICATION NUMBER: JP 8-301429	
; PRIOR FILING DATE: 1996-11-13	
; PRIOR APPLICATION NUMBER: PCT/JP97/04056	
; PRIOR FILING DATE: 1997-11-07	
; NUMBER OF SEQ ID NOS: 91	
; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO 25	
; LENGTH: 372	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
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/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
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/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 288
/ LENGTH: 372
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-205-890-288
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Best Local Similarity 100.0%; Pred. No. 1.8e-187;
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/ Publication No. US2004004835A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C58
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/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
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/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
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/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 288
/ LENGTH: 372
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-208-024-288
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Query Match 100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MKYLRRRRPNATLLIAGAFTLLFSLVSPPTCKVOEOPPAIPBALMPPTTRPAPAP 60
QY 61 CHANTSMVTHDPDPAPOPHVONFLYRHCGRHFPLLQDVPPSKCAQPVFLLVTKSSPSNY 120
DB 61 CHANTSMVTHDPDPAPOPHVONFLYRHCGRHFPLLQDVPPSKCAQPVFLLVTKSSPSNY 120
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DB 121 VRRELLRRTWGRKRGKGLQLRLFLVGTASNPHKRNRLLELAQTHGDILOMPFD 180
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DB 121 VRRELLRRTWGRKRGKGLQLRLFLVGTASNPHKRNRLLELAQTHGDILOMPFD 180
QY 181 SFENLTLKQVFLQWQETRCANASFVLNGDDVFAHTDNMVFYLODHPGRHLFVGQLIQ 240
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QY 241 NVGPTRAFWSKYVPEVVTQNERYPYCGGGGFLSFTAAALRRAAHVLDIFPIDVFL 300
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/ Publication No. US20040053358A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
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;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088722
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088740
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088811
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088825
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKYLRHRRPAAVTLILGAFVTLLESLVSPPTCKVQEOBPAPLPEALAMPPTPTPAPAP 60
Db 1 MKYLRHRRPAAVTLILGAFVTLLESLVSPPTCKVQEOBPAPLPEALAMPPTPTPAPAP 60
Qy 61 CHANTSMVTHPPDPATOPHONFLVYRHCRHPLLDVDPSPKCAOPVFLILVTKSSPSNY 120
Db 61 CHANTSMVTHPPDPATOPHONFLVYRHCRHPLLDVDPSPKCAOPVFLILVTKSSPSNY 120
Qy 121 VRRELLRFTWGRERKVRGIQLRLFLVGTASNPHBAKVNRLLELAQTHGDILOMDFPD 180
Db 121 VRRELLRFTWGRERKVRGIQLRLFLVGTASNPHBAKVNRLLELAQTHGDILOMDFPD 180
Qy 181 SFFNLTIKOVLPIQWERTCANASFLVNGDDVFAHTDNMVFYLODHPGRHLFVGQLIQ 240

```
Db 181 SFFNLTLKQVLFLOMETRCANASFYVINGDDVFAHTDMMVFLYLODHDPGRHLFVGOQLIQ 240
Qy 241 NVGPIRAFMSKYVPEVVTQNERPPYCGGGFLLSFTAAALRAAHVLDIPIDVFL 300
Db 241 NVGPIRAFMSKYVPEVVTQNERPPYCGGGFLLSFTAAALRAAHVLDIPIDVFL 300
Qy 301 GMCLELEGKPAASHSGIRTSQVAPSOHLSSFPDCEFRDILLVHRFLPYEMLLMDALNQ 360
Db 301 GMCLELEGKPAASHSGIRTSQVAPSOHLSSFPDCEFRDILLVHRFLPYEMLLMDALNQ 360
Qy 361 PNLTGNGOTQIY 372
Db 361 PNLTGNGOTQIY 372
```

RESULT 9

```
US-10-176-483-288
; Sequence 288, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-288
```

Query Match 100.0%; Score 2006; DB 12; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.8e-187;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MKYLRRRRPNAATILAIIGAFTLLLSLVSPPTCKVOEOPPAIPBALWPTPTTRAPAP 60
Db 1 MKYLRRRRPNAATILAIIGAFTLLLSLVSPPTCKVOEOPPAIPBALWPTPTTRAPAP 60
Qy 61 CHANTSMVTHPDPATPOHVONFLYRHCRRFPFLDVPSPKCAQVFLLVTKSSPSNY 120
Db 61 CHANTSMVTHPDPATPOHVONFLYRHCRRFPFLDVPSPKCAQVFLLVTKSSPSNY 120
Qy 121 VRELLRRTWGRERKVRGLQLRLFLVGTASNPHARKVNRLLLELAQTHGDILOQDFHD 180
Db 121 VRELLRRTWGRERKVRGLQLRLFLVGTASNPHARKVNRLLLELAQTHGDILOQDFHD 180
Qy 181 SFFNLTLKQVLFLOMETRCANASFYVINGDDVFAHTDMMVFLYLODHDPGRHLFVGOQLIQ 240
Db 181 SFFNLTLKQVLFLOMETRCANASFYVINGDDVFAHTDMMVFLYLODHDPGRHLFVGOQLIQ 240
Qy 241 NVGPIRAFMSKYVPEVVTQNERPPYCGGGFLLSFTAAALRAAHVLDIPIDVFL 300
Db 241 NVGPIRAFMSKYVPEVVTQNERPPYCGGGFLLSFTAAALRAAHVLDIPIDVFL 300
Qy 301 GMCLELEGKPAASHSGIRTSQVAPSOHLSSFPDCEFRDILLVHRFLPYEMLLMDALNQ 360
Db 301 GMCLELEGKPAASHSGIRTSQVAPSOHLSSFPDCEFRDILLVHRFLPYEMLLMDALNQ 360
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```
Qy 361 PNLTGNGOTQIY 372
Db 361 PNLTGNGOTQIY 372
```

RESULT 10

```
US-10-176-749-288
; Sequence 288, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-288
```

Query Match 100.0%; Score 2006; DB 12; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.8e-187;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MKYLRRRRPNAATILAIIGAFTLLLSLVSPPTCKVOEOPPAIPBALWPTPTTRAPAP 60
Db 1 MKYLRRRRPNAATILAIIGAFTLLLSLVSPPTCKVOEOPPAIPBALWPTPTTRAPAP 60
Qy 61 CHANTSMVTHPDPATPOHVONFLYRHCRRFPFLDVPSPKCAQVFLLVTKSSPSNY 120
Db 61 CHANTSMVTHPDPATPOHVONFLYRHCRRFPFLDVPSPKCAQVFLLVTKSSPSNY 120
Qy 121 VRELLRRTWGRERKVRGLQLRLFLVGTASNPHARKVNRLLLELAQTHGDILOQDFHD 180
Db 121 VRELLRRTWGRERKVRGLQLRLFLVGTASNPHARKVNRLLLELAQTHGDILOQDFHD 180
Qy 181 SFFNLTLKQVLFLOMETRCANASFYVINGDDVFAHTDMMVFLYLODHDPGRHLFVGOQLIQ 240
Db 181 SFFNLTLKQVLFLOMETRCANASFYVINGDDVFAHTDMMVFLYLODHDPGRHLFVGOQLIQ 240
Qy 241 NVGPIRAFMSKYVPEVVTQNERPPYCGGGFLLSFTAAALRAAHVLDIPIDVFL 300
Db 241 NVGPIRAFMSKYVPEVVTQNERPPYCGGGFLLSFTAAALRAAHVLDIPIDVFL 300
Qy 301 GMCLELEGKPAASHSGIRTSQVAPSOHLSSFPDCEFRDILLVHRFLPYEMLLMDALNQ 360
Db 301 GMCLELEGKPAASHSGIRTSQVAPSOHLSSFPDCEFRDILLVHRFLPYEMLLMDALNQ 360
Qy 361 PNLTGNGOTQIY 372
Db 361 PNLTGNGOTQIY 372
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RESULT 11

```
US-10-176-914-288
; Sequence 288, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```

; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-288
```

```

Query Match      100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 MKYLRRRPNATLILAI GAFTLLFSLIVSPPTCKVOEOPPAIPALAMPPTPRAPAP 60
DB 1 MKYLRRRPNATLILAI GAFTLLFSLIVSPPTCKVOEOPPAIPALAMPPTPRAPAP 60
QY 61 CHANTSMVTHDPATOPQHVONFLYRHCRRFPLLQDVPPSKCAQPVFLLVIKSSPSNY 120
DB 61 CHANTSMVTHDPATOPQHVONFLYRHCRRFPLLQDVPPSKCAQPVFLLVIKSSPSNY 120
QY 121 VRRELLRRTWGRERKRGQLRLFLVGTASNPHKRNRLLELAQTHGDILOQDFHD 180
DB 121 VRRELLRRTWGRERKRGQLRLFLVGTASNPHKRNRLLELAQTHGDILOQDFHD 180
QY 121 VRRELLRRTWGRERKRGQLRLFLVGTASNPHKRNRLLELAQTHGDILOQDFHD 180
DB 121 VRRELLRRTWGRERKRGQLRLFLVGTASNPHKRNRLLELAQTHGDILOQDFHD 180
QY 181 SFFNLTLLKQVLFLOMOETRCANASFVLANGDDVFAHTDNMFYLODHPGRHLFVGQLIQ 240
DB 181 SFFNLTLLKQVLFLOMOETRCANASFVLANGDDVFAHTDNMFYLODHPGRHLFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVTONERYPPYCGGGFLLSRFTAALRRAAHVLDIPIIDVFL 300
DB 241 NVGPIRAFMSKYVPEVTONERYPPYCGGGFLLSRFTAALRRAAHVLDIPIIDVFL 300
QY 301 GMCLLEGLKPASHSGIRTSQVRAPSOHLSSFPDPCFYRDLIVHRLPYEMLMMDALNQ 360
DB 301 GMCLLEGLKPASHSGIRTSQVRAPSOHLSSFPDPCFYRDLIVHRLPYEMLMMDALNQ 360
QY 361 PNLTCGNQTOIY 372
DB 361 PNLTCGNQTOIY 372
```

RESULT 12
US-10-176-915-288

```

; Sequence 288, Application US/10176915
; Publication No. US2003001754A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jjian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/176,915
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-288
```

```

Query Match      100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 MKYLRRRPNATLILAI GAFTLLFSLIVSPPTCKVOEOPPAIPALAMPPTPRAPAP 60
DB 1 MKYLRRRPNATLILAI GAFTLLFSLIVSPPTCKVOEOPPAIPALAMPPTPRAPAP 60
QY 61 CHANTSMVTHDPATOPQHVONFLYRHCRRFPLLQDVPPSKCAQPVFLLVIKSSPSNY 120
DB 61 CHANTSMVTHDPATOPQHVONFLYRHCRRFPLLQDVPPSKCAQPVFLLVIKSSPSNY 120
QY 121 VRRELLRRTWGRERKRGQLRLFLVGTASNPHKRNRLLELAQTHGDILOQDFHD 180
DB 121 VRRELLRRTWGRERKRGQLRLFLVGTASNPHKRNRLLELAQTHGDILOQDFHD 180
QY 181 SFFNLTLLKQVLFLOMOETRCANASFVLANGDDVFAHTDNMFYLODHPGRHLFVGQLIQ 240
DB 181 SFFNLTLLKQVLFLOMOETRCANASFVLANGDDVFAHTDNMFYLODHPGRHLFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVTONERYPPYCGGGFLLSRFTAALRRAAHVLDIPIIDVFL 300
DB 241 NVGPIRAFMSKYVPEVTONERYPPYCGGGFLLSRFTAALRRAAHVLDIPIIDVFL 300
QY 301 GMCLLEGLKPASHSGIRTSQVRAPSOHLSSFPDPCFYRDLIVHRLPYEMLMMDALNQ 360
DB 301 GMCLLEGLKPASHSGIRTSQVRAPSOHLSSFPDPCFYRDLIVHRLPYEMLMMDALNQ 360
QY 361 PNLTCGNQTOIY 372
DB 361 PNLTCGNQTOIY 372
```

RESULT 13
US-10-176-484-288

```

; Sequence 288, Application US/10176484
; Publication No. US20030059876A9
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jjian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C64
; CURRENT APPLICATION NUMBER: US/10/176,484
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-484-288
```


Query Match 100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRPVATLILAIIGFTLLLSLVSPPTCKVOEOPPAIPEALAMPPTPTRAPAP 60
DB 1 MKYLRRRPVATLILAIIGFTLLLSLVSPPTCKVOEOPPAIPEALAMPPTPTRAPAP 60
QY 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120
DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120
QY 121 VREELLRRTWGRERKVRGLQRLFLVGTASNHEARKVNRILLEAQTGDILOQDFHD 180
DB 121 VREELLRRTWGRERKVRGLQRLFLVGTASNHEARKVNRILLEAQTGDILOQDFHD 180
QY 181 SFFNLTLKQVLFLOMETRCANASFVINGDDVFAHTDMNVFYLQDHPGRHLFVGQLIQ 240
DB 181 SFFNLTLKQVLFLOMETRCANASFVINGDDVFAHTDMNVFYLQDHPGRHLFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIPIDVFL 300
DB 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIPIDVFL 300
QY 301 GMLLEGLKPAHSGIRTSGVAPSOHLSPDCFYRDLILVHRFLPYEMLLMDALNQ 360
DB 301 GMLLEGLKPAHSGIRTSGVAPSOHLSPDCFYRDLILVHRFLPYEMLLMDALNQ 360
QY 361 PNLTGNGQTOIY 372
DB 361 PNLTGNGQTOIY 372

RESULT 14
US-10-180-550-288
; Sequence 288, Application US/10180550
; Publication No. US20030064440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-180-550-288

Query Match 100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRPVATLILAIIGFTLLLSLVSPPTCKVOEOPPAIPEALAMPPTPTRAPAP 60
DB 1 MKYLRRRPVATLILAIIGFTLLLSLVSPPTCKVOEOPPAIPEALAMPPTPTRAPAP 60
QY 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120
DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120

DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120
QY 121 VREELLRRTWGRERKVRGLQRLFLVGTASNHEARKVNRILLEAQTGDILOQDFHD 180
DB 121 VREELLRRTWGRERKVRGLQRLFLVGTASNHEARKVNRILLEAQTGDILOQDFHD 180
QY 181 SFFNLTLKQVLFLOMETRCANASFVINGDDVFAHTDMNVFYLQDHPGRHLFVGQLIQ 240
DB 181 SFFNLTLKQVLFLOMETRCANASFVINGDDVFAHTDMNVFYLQDHPGRHLFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIPIDVFL 300
DB 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIPIDVFL 300
QY 301 GMLLEGLKPAHSGIRTSGVAPSOHLSPDCFYRDLILVHRFLPYEMLLMDALNQ 360
DB 301 GMLLEGLKPAHSGIRTSGVAPSOHLSPDCFYRDLILVHRFLPYEMLLMDALNQ 360
QY 361 PNLTGNGQTOIY 372
DB 361 PNLTGNGQTOIY 372

RESULT 15
US-10-183-014-288
; Sequence 288, Application US/10183014
; Publication No. US20030064441A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C170
; CURRENT APPLICATION NUMBER: US/10/183,014
; CURRENT FILING DATE: 2002-06-26
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 288
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-183-014-288

Query Match 100.0%; Score 2006; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-187;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLRRRPVATLILAIIGFTLLLSLVSPPTCKVOEOPPAIPEALAMPPTPTRAPAP 60
DB 1 MKYLRRRPVATLILAIIGFTLLLSLVSPPTCKVOEOPPAIPEALAMPPTPTRAPAP 60
QY 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120
DB 61 CHANTSMVTHPDPATOPQHVONFLYRHCNHPFLQDVPSPKCAQVFLLVKSSPSNY 120
QY 121 VREELLRRTWGRERKVRGLQRLFLVGTASNHEARKVNRILLEAQTGDILOQDFHD 180
DB 121 VREELLRRTWGRERKVRGLQRLFLVGTASNHEARKVNRILLEAQTGDILOQDFHD 180
QY 181 SFFNLTLKQVLFLOMETRCANASFVINGDDVFAHTDMNVFYLQDHPGRHLFVGQLIQ 240
DB 181 SFFNLTLKQVLFLOMETRCANASFVINGDDVFAHTDMNVFYLQDHPGRHLFVGQLIQ 240
QY 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIPIDVFL 300
DB 241 NVGPIRAFMSKYVPEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIPIDVFL 300

Db	241	NVGPIRAFWSKYYVEVWTQNERYPYCGGGFLLSRFTAALRRRAHVLDIFPIDVFL	300
Qy	301	GMCLLEBGLKPAHSHGIRTSQVRAPOHLSFDPCEYRDLLVHRFLPYEMLLMDALNQ	360
Db	301	GMCLLEBGLKPAHSHGIRTSQVRAPOHLSFDPCEYRDLLVHRFLPYEMLLMDALNQ	360
Qy	361	PNLTGNGNOTQIY	372
Db	361	PNLTGNGNOTQIY	372

Search completed: June 14, 2004, 13:53:38
Job time : 49 secs

protein T24P13.20 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: F86394
R/Theologian: A.E. Ecker, J.R. Palm, C.J. Federspiel, N.A. Kaul, S. White, O. Alonso
Chin, C.W., Chung, M.K., Conn, L., Conway, A.B., Conway, A.R., Creasy, T.H., Dewar, K.
ansen, N.F., Hughes, B., Hultzar, L.
A/Authors: Hunter, J.L., Jenkins, J., Johnson-Hopson, C., Khan, S., Khaykin, E., Kim, C.
Rizzo, M., Rooney, T., Rowley, D., Sakano, H.
C.A., Li, J.H., Li, Y., Lin, X., Liu, S.X., Liu, Z.A., Luoro, J.S., Maiti, R., Marzialis,
A. Authors: Salzberg, S.L., Schwartz, J.R., Shinn, P., Southwick, A.M., Sun, H., Tallon,
ker, M., Wu, D., Yi, G., Fraser, C.M., Venter, J.C., Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A66141; MUID:21016719; PMID:11130712
A/Accession: F86394
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-684 <STO>
A/Cross-references: GB:AE005172; NID:g9295733; PIDD:AAF87039.1; GSPDB:GN00141
C/Genetics:
A/Gene: T24P13.20
A/Map position: 1

	Query Match	11.3%	Score 226;	DB 2;	Length 684;
	Best Local Similarity	26.5%;	Pred. No. 8,7e-12;		
	Matches	75;	Conservative 54;	Mismatches 102;	Indels 54; Gaps 9
QY	105 QPWFLLLVIKSSPSNYRRELLRTKRWGRKKRGQLRLFLVLTAGSPHFAKVRNLE	164			
Db	409 RPDLIVYGFSTANNPKRRMAVRRTWQYDVSRAVRFVGL-----HKSLPVNLELM	464			
QY	165 LEAQTGGDILQMWFHSFENLTLKV-----LFQMETFCAASPYVLNG	209			
Db	465 NEARTGYDVQMLPFUDYYLSLMTKTALICIFGSLSYCPASLYSFQTEVDNAKFIIMKT	524			
QY	210 DDDVFPAHTDNMFYLQDDHPGHSLFVGQLIQNVGPIRAFWSKYVV-----PEVV	258			
Db	525 DDDAFPRVBEVLLSMTNTNTGILLYGINSIDOPIRNDPSKMVIYSYELFKKEWPE--	582			
QY	259 TONERYPYPCGGGGFLSRFTAAALBRAAH--LDIPFDVPLGMG---LELEGKPPAS	313			
Db	583 ---EKFPMAHGPGYIVSRDIALSESGFKFGKNLKMFLIEDVANAGIATIAETLTHGLEPHY	639			
QY	314 HSGIRTSGYRABSQHLSFDFCFYTD-LLVLRFLPYBMLIMW	355			
Db	640 ENDGRITIS-----DGC--KDGVVAHYOSPAMETCLW	669			

RESULT 3
 D96777
 hypothetical protein F25A4.23 [imported] - Arabidopsis thaliana
 (Species: Arabidopsis thaliana (mouse-ear cress))
 C|Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C|Accession: D96777
 R|Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
 ansen, N.F.; Hughes, B.; Huzar, L.
 Nature 408, 816-820, 2000
 A|Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzall,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A|Authors: Saldegy, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A|Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A|Reference number: A86141; MUID:21016719; PMID:11130712
 A|Accession: D96777
 A|Status: preliminary
 A|Structure type: DNA
 A|Residues: 1-642 <STD>
 A|Cross-references: GB:AE05173; NID:55882743; PIDN:AD55296.1; GSPDB:GN00141
 C|Genetics:
 A|Gene: F25A4.23
 A|Map position: 1

[illegible]

RESULT 4
 T18639
 hypothetical protein B0024.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/accession: T18639
 R:McMurray, A.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z19001
 A:Accession: T18639
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-507 <WIL>
 A:Cross-references: EMBL:Z71178; PIDD:CAA94876.1; GSPDB:GN00023; CESP:B0024.3
 A:Experimental source: Clone B0024
 C:Genetics:
 A:Gene: CESP:B0024.3
 A:Map position: 5
 A:introns: 69/2; 118/2; 143/2; 181/1; 246/2; 281/3; 393/2; 437/3

	Query Match	10.9%	Score 218.5	DB 2	Length 507
	Best Local Similarity 24.3%		Pred. No. 2.7e-11		
	Matches 63	Conservative 52	Mismatches 119	Indels 25	Gaps 6
QY	64	NTSWTHPDPAFQPOHVNFLLRHCRHFFLLDVPSPSKAQPVFLLVIKSSPSNVYR	123		
-Db	218	STNCPYHAQFQDQ-NHTYQFI-----TVPKKQCSNNRKLQTTILSTAGNFDR	264		
QY	124	ELLRFTW---GRERKVRGLQRLRLFLVIGTASNPHPEARVNNLLLEAQTHDILLQWPHD	180		
-Db	265	QAIKETMANPNNSSEHVANNVDIRIFITLSKTSNEF---LNFALQRELEKPDMMVTLDYE	320		
QY	181	SPFNULTKQVLFLOMQETRCANASFLVINGDDVDVAHTDNNVFYLLQDHPGRHLEFVGQLI-	239		
-Db	321	SYELLILKVAHLISYKQSHCOLAFQKCIDDDMAVMDMGVRSLEDKQASINGISGIW	380		
QY	240	QNVGPIRAFNGKYVYEVVTQENERYPPYCGGGGLLSRFTAALRAAHVLDIPFDVF	299		
-Db	381	KNSPFVAKKGRWVYFKLISEKFPFYIDQPIYLIGNAVPRMLEKKNQNTIEDVF	440		
QY	300	---LGMCLLEGLKLPASH	314		
-Db	441	WTGVIGALKATKQIINMANH	459		

RESULT 5

hypothetical protein T15D6.5 - *Caenorhabditis elegans*C1:Species: *Caenorhabditis elegans*

C1:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C1:Accession: T24925

R. Dobson, R. submitted to the EMBL Data Library, November 1996

A:Reference number: Z19956

A:Accession: T24925

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-376 <WIL>

A:Cross-references: EMBL:Z83125; PIDN:CA05616.1; GSPDB:GN00019; CESP:T15D6.5

A:Experimental source: clone T15D6

C:Genetic:

A:Gene: CESP:T15D6.5

A:Map position: 1

A:Introns: 59/1; 87/1; 207/3; 274/2; 316/3; 339/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match

10.2%; Score 204; DB 2; Length 376;

Best Local Similarity 24.4%; Pred. No. 3.6e-10;

Matches 66; Conservative 56; Mismatches 119; Indels 30; Gaps 10;

QY 91 HFFLLDDVPPSKCAQVF--LLVTKSSPSNVYRELRTW---GREKVRGLQRL 144

DB 115 HLP-----KIKNPTWMDILMIVASRGVSRRVLRKTMNKNANSKTIINGRQVL 166

QY 145 FLVGTASNPHEARKVRLLEBAQTGDIQMPFHSFPLTLKQVLFLOMQETRCANAS 204

DB 167 FLVGMVAGBRDLMA---VKKEASFGDITVNLLEDITDLPKVLISLLYGNKASDFK 223

QY 205 FVLNGDDVFAHTDNVFLQDH--DGRHLFVQGLIQNVG--PIRAFWSKRYVEVVTQN 261

DB 224 IIGKIDDDVIFPPDRITPLIDENVIDSSYSYIGVLSQDELIVRNETKPMVYPERAVNC 283

QY 262 ERPPYCGGGFLSFTAAALRRAAVLDIPIDVFLGMCLEGLKPAHS--GIRTS 320

DB 284 TKKPVVALGPFYLLITKAAALIVENSFQNFMTVEEDALAGII--ASGLGIQRHSLPMNTD 342

QY 321 GVRAFSQHLSS-----FDPCCFYRDLVLVHR 345

DB 343 GKILSWHMSKSDROPLD--FYQSLALYQ 371

RESULT 6

T20028

hypothetical protein C47F8.5 - *Caenorhabditis elegans*C1:Species: *Caenorhabditis elegans*

C1:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C1:Accession: T20028

R. McLeay, K. submitted to the EMBL Data Library, December 1997

A:Reference number: Z19212

A:Accession: T20028

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-332 <WIL>

A:Cross-references: EMBL:AL009246; PIDN:CA015838.1; GSPDB:GN00019; CESP:C47F8.5

A:Experimental source: clone C47F8

C:Genetic:

A:Gene: CESP:C47F8.5

A:Map position: 1

A:Introns: 26/1; 146/3; 213/2; 255/3; 285/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match

9.9%; Score 198.5; DB 2; Length 332;

Best Local Similarity 24.2%; Pred. No. 9.3e-10;

Matches 63; Conservative 51; Mismatches 107; Indels 39; Gaps 8;

QY 109 LLVTKSSPSNVYRELRTWGRKK---VRGLQRLFLVGTASNPHEARKVRLLEL 165

DB

67 ILMMVASRTDSEFARRVLRKTMNKNYSIIVRGRRKALFLVGMVS---EDYVRRIVME 123

QY 166 EAQTHGDIQMPFHSFPLTLKQVLFLOMQETRCANASFLVNGDDVFAHTDNMVFYQ 225

DB 124 EAKLYDMDVVIDLEDYDPLPFKSLISLLYVASKAEFFKVIKIDBDWFPPLKLP 183

QY 226 DH--DGRHLFVQGLIQNVGPI---RAFWSKRYVEVVTQNBRYPYCGGGFLSFRFT 279

DB 184 GKVIDPDAAFYQQLKEGEFVYKKQDAH---YVDYVANCYRAYVAGPFYLATRKA 240

QY 280 AALRRRAAVLIDIPIDVFLGMCLEGLKPAHSIGRTSGVRAFSQHLSSFDPCFY-- 337

DB 241 AKLVKFTKQNMTVEDSLI-----TGILANDGIPRKNLEHYRHDYDI 286

QY 338 -----RDLVLVHRF---LPI 349

DB 287 QDNEGKEILLAMHSFKNNIPY 306

RESULT 7

G86397

protein TN9.18 (imported) - *Arabidopsis thaliana*C1:Species: *Arabidopsis thaliana* (mouse-ear cress)

C1:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C1:Accession: G86397

R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

Nansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Malt, R.; Marziani

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MID:21016719; PMID:11130712

A:Accession: G86397.

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-657 <STO>

A:Cross-references: GB:AB005172; NID:g8778858; PIDN:AAF79857.1; GSPDB:GN00141

C:Genetic:

A:Gene: TN9.18

A:Map position: 1

Query Match

9.9%; Score 198.5; DB 2; Length 657;

Best Local Similarity 24.6%; Pred. No. 2.2e-09;

Matches 74; Conservative 52; Mismatches 114; Indels 61; Gaps 11;

QY 69 THDPATOPQHVONFLYHCHRFLLQDVPPSKCAQVPLLVTKSSPSNVYRELRT 128

DB 399 TNSFAPQ-KHLEMRWK-----ASLPPKP-----RAAVRK 430

QY 129 TWGRERKVGLOLRLFLVGTASNPHEARKVRLLEBAQTHGDIQMPFHSFPLTLK 188

DB 431 SMQOKLVRSSKVAFAFVAL---HARKEVNDLKEAEYRGDITVYPMIDYDLVTK 486

QY 189 OVLFWOETRCANASFLVNGDDVFAHTDNVFLQDHPGRHLFVQGLIQNVGIRAP 248

DB 487 TVALICEGVNTVA--AKYVKKDDDTFVRDAVIGAEKVGKGRSLYIGNINFHKLRT-- 544

QY 249 WSKTYVPEVVTQNERPPYCGGGFLSFTAAAL-----RAAVLIDIPIDVFLGM 302

DB 545 -GKMAVTFEWEVEEYVPYANGPGYLLSYDAKFIYDDEOKR-----LRLFKMEDVSMG 599

QY 303 CLEBGLKPAHSIGRTSGVRAFSQHLSSFDPCFY--RDLVLVHRFLPYEMLLAMDALN 359

DB 600 WVE-----KFNETR--PVAVVHSLKFCQFCIEDYFRAHQSRQMICMDXKO 646

QY 360 Q 360

DB 647 R 647

RESULT 8

T20876

hypothetical protein F14B6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C/Accession: T20876

R/White, S.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19338

A/Accession: T20876

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-376 <WIL>

A/Cross-references: EMBL:Z81502; PIDN:CAB04107.1; GSPDB:GN00019; CESP:F14B6.4

A/Experimental source: clone F14B6

C/Genetics:

A/Gene: CESP:F14B6.4

A/Map position: 1

A/Introns: 31/1; 69/1; 189/3; 256/2; 298/3; 328/3

C/Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1

Query Match 9.4%; Score 189; DB 2; Length 376;

Best Local Similarity 24.4%; Pred. No. 7.5e-09;

Matches 58; Conservative 51; Mismatches 101; Indels 28; Gaps 8;

QY 109 LLLVKSPPSNVYRRLRLRTMGREK--VRGLQRLFLVVG-TASNPEARKVNRLL 164

Db 109 LLMIVASRTDSFARRVAVLAKTMNPNSEIIDGRKALFLVGMTDGDSSRRKV--VME 166

QY 165 LERQTHGDIQMDPHDSFNNLTIKQVLFQWQETRCANASFYVNGDDVFAHTDMVFYL 224

Db 167 -EARIYGDVVVVDLKDYEELPFKSLTTLTGTSKASEFKLIGKIDEDIMFPDKILPL 225

QY 225 QDH--DPGRHLFFGOLIQVVGPI-RAFMKYYVPEVTVQNERPPYCGGGFLSRFPA 281

Db 226 EQNLIDPSESEIYGMFLFAGGIVYNDKEHMFVPOSTYGCDFPPYTGGLFYLVTQDAK 285

QY 282 ALRRAAVLIDIPIDVFLGMCLLEGLKPAHSGIRTSGVAPFQHLSPFCFYRD 339

Db 286 KLIMATKRIFFIPEDAL-----NGLNANDCKIRIHL-----PELYGD 325

RESULT 9

T20029

hypothetical protein C47F8.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C/Accession: T20029

R/McLay, K.

submitted to the EMBL Data Library, December 1997

A:Reference number: Z19212

A/Accession: T20029

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-357 <WIL>

A/Cross-references: EMBL:AL009246; PIDN:CAI5839.1; GSPDB:GN00019; CESP:C47F8.6

A/Experimental source: clone C47F8

C/Genetics:

A/Gene: CESP:C47F8.6

A/Map position: 1

A/Introns: 19/1; 52/1; 172/3; 239/2; 281/3; 311/3

C/Superfamily: Caenorhabditis elegans hypothetical protein T09F5.1

Query Match 9.4%; Score 188.5; DB 2; Length 357;

Best Local Similarity 22.8%; Pred. No. 7.8e-09;

Matches 62; Conservative 49; Mismatches 98; Indels 63; Gaps 10;

QY 109 LLLVKSPPSNVYRRLRLRTM--GRRKRYGQLRLFLVVGTAHPHARKVNRLL 165

Db 93 LLMIVASRTDSFARRNIRQTWNKNSSEIVANGRKSLFLVGLAPADY--KVKKVMQ 149

QY 166 EAQTHGDIQMDPHDSFNNLTIKQVLFQWQETRCANASFYVNGDDVFAHTDM-VFYL 224
Db 150 EAKLYGDIIVYMDTYEELIYKSLIMIFLFGVSKAPQYKTIKIDEDIMFPDKLMALYE 209
QY 225 Q--DHP-----GRHLFVQGLQVNGPIRAFMSKYYVPEVTVQNERPPYCGGG 271
Db 210 QGIIISTVSLYGLVPIAGRDIF-----RDKTRNRYVPEASVSCSQPAYLSGM 258
QY 272 GFLLSRFTAALRAAHVLDIPIDVFLGMCLLEGLKPAHSGIRTSGVAPFQHLSS 331
Db 259 YVMATREAAQMLKSTKGRDFIQVEDVL-----TGLAEDGIRIDM-- 302
QY 332 FDPCTY-----RDLLVHRF--LPY 349
Db 303 --PKLYKPPHDIKKNDNDIIMAHNYKNPIY 332

RESULT 10

T20203

hypothetical protein C54C8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T20203

R/Dobson, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19237

A/Accession: T20203

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-262 <WIL>

A/Cross-references: EMBL:Z81502; PIDN:CAB05465.1; GSPDB:GN00019; CESP:C54C8.3

A/Experimental source: clone C54C8

C/Genetics:

A/Gene: CESP:C54C8.3

A/Map position: 1

A/Introns: 19/2; 117/3; 184/2; 226/3

Query Match 9.0%; Score 181.5; DB 2; Length 262;

Best Local Similarity 22.9%; Pred. No. 2.2e-08;

Matches 58; Conservative 57; Mismatches 97; Indels 41; Gaps 9;

QY 79 HVONFLLYRHC-----HFPLLDVPPSKCAQVFLLVVKSPPSNVYRRLRTM---G 131

Db 9 HLKLIKILARNLYSWLYLPEIET-----SQEKDILIVASRTDSFARRNIRQTWNKSKA 63

QY 132 RRRYRGLQRLFLVVGTAHPHARKVNRLELEAQTHGDIQMDPHDSFNNLTIKQV 191

Db 64 NSEIVANGRMKPLFLVGLTPGEY--KMKVMVQBEAKLYGDIIVDMNDNYEELTYKSLA 120

QY 192 FLOWETRCANASFYVNGDDVFAHTDMVFYLODHPGRHLFVQGLQVNGPIRAFMSK 251

Db 121 ILVGVSKAPRYGMICKIDEDVFPDKLT--ELYDQ--FT-----DAPPLRYGAK 169

QY 252 -----YVPEVTVQNERPPYCGGGFLSRFAALRAAHVLDIPID 297

Db 170 MOSGANIFRDKTRHMYVPESSVSCSKFPEYVGMVYVWBAQQIKSTKTRDFIQVED 229

QY 298 VFL--GMCLLEGL 309

Db 230 VFLTGILAEDEL 242

RESULT 11

T20446

hypothetical protein E03H4.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C/Accession: T20446

R/Dobson, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19276

A/Accession: T20446

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-384 <M1>
A:Cross-references: EMBL:Z81492; P1DN:CAB04032.1; GSPDB:GN00019; CESP:E03H4.11
A:Experimental source: clone E03H4
C:Genetics:
A:Gene: CESP:E03H4.11
A:Map position: 1
A:introns: 46/1; 76/1; 196/3; 263/2; 305/3; 335/3
C:superfamily: Caenorhabditis elegans hypothetical protein T09F5.1

Query Match 8.8%; Score 176; DB 2; Length 384;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
Matches 52; Conservative 50; Mismatches 92; Indels 32; Gaps 5;

Oy 102 KCAQVFLILVYKSSPSNVYRRELLIRRTWGERK---VRGLQRLILFLVGRASNPHEARK 158
Db 110 EASQEKDILMTIVASRTDYSARRNRIRQTWNKSDSEIYANGMKLFLVGLTPGDY---K 166
Oy 159 VNRLLLEAQTGHGDLQMDPFHSFENLILTKQVLFQMOETRCANASFLVANGDDVFAHTD 218
Db 167 MKKVMQGAKLXGLDIIVDNDVTYELLYKSLAILLYGVSKAPRQMTGKIDEDVIFPPD 226
Oy 219 NMVFLQDHPGRHLFVQLIQNVGPIRPFMSK-----YYVEVYTONERY 264
Db 227 KLIALYE-----QGIIIDATPLCAYGYKIQAGARIFRDKNDRWYVSSYSCSF 275
Oy 265 PRYCGGGFLLSRFTAAALRRAPAHVLDIFPIDVFL-GMCLEBGL 309
Db 276 PEYVSGMLYMTWENAQQIISTKYRDFIOVEDVFLTGLIABDLGI 321

RESULT 12
T20031
hypothetical protein C47F8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T20031; T22806
R:McLay, K.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z19212
A:Accession: T20031
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-345 <M1>
A:Cross-references: EMBL:AL009246; P1DN:CA15841.1; GSPDB:GN00019; CESP:C47F8.3
A:Experimental source: clone C47F8
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19617
A:Accession: T22806
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-345 <M1>
A:Cross-references: EMBL:Z81553; P1DN:CAB04502.1; GSPDB:GN00019; CESP:C47F8.3
A:Experimental source: clone F56H6
C:Genetics:
A:Gene: CESP:C47F8.3
A:Map position: 1
A:introns: 23/1; 49/1; 169/3; 236/2; 278/3; 308/3
C:superfamily: Caenorhabditis elegans hypothetical protein T09F5.1

Query Match 8.3%; Score 167; DB 2; Length 345;
Best Local Similarity 22.4%; Pred. No. 5.8e-07;
Matches 56; Conservative 51; Mismatches 117; Indels 26; Gaps 7;

Oy 109 LILVYKSSPSNVYRRELLIRRTWGERK---VRGLQRLILFLVGRASNPHEARKVRLLEL 165
Db 90 ILMLVVSSTKIPFARNVIRSTWMNKENSEMKSGRHALLFFVGLIPGDQNLKTL--VLE- 146
Oy 166 EAQTHGDLQMDPFHSFENLILTKQVLFQMOETRCANASFLVANGDDVFAHTDNNVFLQ 225
Db 147 EAEIHGDVVVDLEDITVDNLEPFTALILYGTSSKASQRIKIGDKIDVDVFPDQLPMLD 206

Qy 226 DHDPRHFLVFGQLIONVG-----PIRAFWSKYVEEVYQNRYPYCGGGFLSR 277
Db 207 -----RNVNNTSLISYHGLSTAEELVLRNKEPYVEETANCYVPPYVNGPIYLTVRK 261

Qy 278 FTAALRRRAHYLDIPIDVFL-GMCLEBLEGKPAK-----HSGIRTSGYRABSOHLS 330
Db 262 DAASILDNANHQCMTVEDALITGIIAQKIGIRRYSLPNVFRHRNDITEGODVLAMHVQ 321

Qy 331 SFDPCFYRDL 340
Db 322 TKNDSEYKSI 331

RESULT 13
T24762
hypothetical protein T09F5.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T24762
R:Mortimore, B.
submitted to the EMBL Data Library, December 1996
A:Reference number: 219933
A:Accession: T24762
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-325 <MIL>
A:Cross-References: EMBL:283339; PIDN:CAB05807.1; GSPDB:GND00023; CESP:T09F5.1
A:Experimental source: clone T09F5
C:Genetic8:
A:Gene: CESP:T09F5.1
A:Map position: 5
A:introns: 19/1; 155/3; 223/2; 265/3
C:Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 7.4% Score 149; DB 2; Length 325;
Best Local Similarity 24.3%; Pred. No. 2, 1e-05;
Matches 55; Conservative 39; Mismatches 84; Indels 48; Gaps 8;

Qy 109 LLVIVKSSPSNVYRELLRTWGRKVRGQLRLPLVGTASNPHEARKVRLLELEAQ 168
Db 81 ILLIITSRPDDFSRNNAIKRTWMNQKT--NQITSFVMVGLSSKTKDE--KVADIVMREAR 135

Qy 169 THGDIQMDHFDSPFNLLKQVLPFQNETRCANSPV--LNGD-----DD 212
Db 136 LYRDIIVTSLBDSYTKLAFKTLSTLLVAVSKRPSQQLIGRVDGDLFPENLFOGFLDKDN 195

Qy 213 VFAHTDNVNFYQLQDHPGRHLFVGGIIONVGPFRAPWSKYVYPRVVTQNERYPYC----- 268
Db 196 YFINTNNSIY-----GYIABEGKPTTSKCK-----SRFLFPFKCSNYL 236

Qy 269 ---GGGCFLLSRFTAAALRRRAHYLDIPID-VELGMCLEBLEGLK 310
Db 237 SFLSPFFLLTRPAEKLLNLSKRRHDFHQIDQLITGGMADAGYK 282

RESULT 14
A66186
hypothetical protein [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A66186
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiehl, N.A.; Kaul, S.; White, O.; Alonso-Blanco, C.; Wehner, J.; Schuster, J.R.; Schuster, C.M.; Venter, J.C.; Davis, R.W.; Chinn, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marshall, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, B.; M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: A66186

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OM protein - protein search, using sw model

Run on: June 14, 2004, 13:29:32 ; Search time 17 Seconds

(without alignments)
1139.418 Million cell updates/sec

Title: US-10-019-735-2

Perfect score: 2006

Sequence: 1 MXYLHRRNPATLILAGAF.....LMMDALNQNLTGNGOTQIY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	100.0	372	1 B3G8_HUMAN	O9y2a9 h beta-1,3-
2	601	30.0	397	1 B3G7_HUMAN	O9ny97 h beta-1,3-
3	416	20.7	300	1 B3G5_GORGO	O9n293 g beta-1,3-
4	416	20.7	310	1 B3G5_HUMAN	O9n293 h beta-1,3-
5	413	20.6	301	1 B3G5_PANPA	O9n294 p beta-1,3-
6	402	20.0	297	1 B3G5_PANTR	O9n295 p beta-1,3-
7	377	18.8	308	1 B3G5_MOUSE	O9j167 m beta-1,3-
8	312	15.6	378	1 B3G4_HUMAN	O96024 homo sapien
9	298.5	14.9	371	1 B3G4_RAT	O88178 rattus norv
10	298	14.9	371	1 B3G4_MOUSE	O92060 mus musculu
11	129	6.4	573	1 SECD_MYCTU	O50634 mycobacteri
12	99.5	5.0	331	1 RFNG_HUMAN	O9y644 homo sapien
13	95.5	4.8	412	1 FNG_DROME	O24342 drosophila
14	95.5	4.8	761	1 PQOF_KLEPN	P27508 klebsiella
15	95	4.7	832	1 DPOL_HPBVA	P240024 hepatitis b
16	95	4.7	1375	1 BNRI_YEAST	P40450 saccharomyc
17	94	4.7	503	1 SYK_NEIMA	O9j1c7 neisseria m
18	93.5	4.7	379	1 LFNG_HUMAN	O8ne33 homo sapien
19	92	4.6	503	1 SYK_NEIMA	O9j1y6 neisseria m
20	90.5	4.5	962	1 Y4E_SCHPO	O09771 schizosacch
21	90.5	4.5	1698	1 CUL1_HUMAN	O14999 homo sapien
22	89.5	4.5	265	1 IHA_SHEEP	P38440 ovis aries
23	88.5	4.4	308	1 JUNE_CYPFA	P79703 cyprinus ca
24	88	4.4	750	1 DPOL_HPBVA	P03155 hepatitis b
25	87.5	4.4	960	1 VP41_LYCES	P93221 lycopersico
26	86.5	4.3	2236	1 PYRI_DROME	P05990 drosophila
27	86	4.3	970	1 K852_HUMAN	O9y6c9 homo sapien
28	86	4.3	2482	1 VMP_PIG	O28883 sus scrofa
29	85.5	4.3	2813	1 VWF_CANPA	O28825 canis famli
30	85	4.2	724	1 P85A_BOVIN	P23737 bos taurus
31	85	4.2	2715	1 ML14_HUMAN	O9um66 homo sapien
32	84	4.2	202	1 VIC2_AGRRH	P13460 agrobacteri
33	84	4.2	389	1 THS3_ARABY	P51069 arabidops hyp

34	83.5	4.2	519	1 VL2_HPV14	P36749 human papil
35	83.5	4.2	1239	1 NME3_MOUSE	O01098 mus musculu
36	83.5	4.2	2813	1 VWF_HUMAN	P04275 homo sapien
37	83	4.1	370	1 RECF_LISTIN	O92f08 listeria in
38	83	4.1	370	1 RECF_LISTIN	O92f08 listeria in
39	83	4.1	371	1 HEM2_RALSO	O8xw32 ralteconla s
40	83	4.1	597	1 V70K_OYMV	P20130 ononis yell
41	83	4.1	1123	1 V120_HSV11	P10221 herpes simp
42	82.5	4.1	202	1 VIC2_AGRTS	P07166 agrobacteri
43	82.5	4.1	402	1 GBA1_TRIVA	O86486 trichomonas
44	82.5	4.1	730	1 CDK9_CAEEL	P46531 caenorhabdi
45	82.5	4.1	1034	1 CAP6_SYNY3	P74299 synchocyst

ALIGNMENTS

RESULT 1
B3G8_HUMAN STANDARD; PRT; 372 AA.
AC O9Y2A9;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-1,3-galactosyltransferase 8 (EC 2.4.1.-) (Beta-1,3-GalTase 8)
DE (Beta3Gal-T8) (UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase 8) (UDP-gal:beta-GlcNAc beta-1,3-N-DE galactosyltransferase 8) (Beta-3-GX-T8) (Core 1 extending beta-1,3-N-DE acetylglucosaminyltransferase) (Core1-beta3GlcNAcT).
GN B3GNT3 OR B3GALT8 OR TMEM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=99173880; PubMed=10072769;
RA Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
RT "selection of cDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.";
RL Cell 228:161-167(1999).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21332592; PubMed=11439191;
RA Yeh J., Hiraoka N., Petryniak B., Nakayama J., Ellices L.G., Rabuka D.,
RA Hindsgaul O., March J.D., Lowe J.B., Fukuda M.;
RT "Novel sulfated lymphocyte homing receptors and their control by a core1 extension beta1,3-N-acetylglucosaminyltransferase.";
RL Cell 105:957-969(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20047730; PubMed=10580128;
RA Amado M., Almeida R., Schwiens T., Clausen H.;
RT "Identification and characterization of large galactosyltransferase gene families: galactosyltransferases for all functions.";
RL Biochim. Biophys. Acta 1473:35-53(1999).
RN [4]
RP REVIEW.
RX MEDLINE=20047730; PubMed=10580128;
RA Amado M., Almeida R., Schwiens T., Clausen H.;
RT "Identification and characterization of large galactosyltransferase gene families: galactosyltransferases for all functions.";
RL Biochim. Biophys. Acta 1473:35-53(1999).
RN [5]
RP FATHYMA; Glycosylation.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
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CC EMBL; AB015630; BAA76497.1; -.
DR EMBL; AF293973; AAK00849.1; -.
DR EMBL; AJ130847; CAC45044.1; -.
DR Gene; HGNC:13528; B3GNT3.
GO; GO:0005887; C:integral to plasma membrane; TAS.
DR InterPro; IPR002659; Glyco trans_31.
DR Pfam; PF01762; Galactosyl_T; 1.
KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
KM Signal-anchor; Golgi stack; Multigene family.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 32 372 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA; 42515 MW; A6B3FB88AFCCFC2 CRC64;

Query Match 100.0%; Score 2006; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLHRRRNATLLAIGAFLLLFSLVSPPTCKVQEQPPAIPALAMPPTPPAPAP 60
DB 1 MKYLHRRRNATLLAIGAFLLLFSLVSPPTCKVQEQPPAIPALAMPPTPPAPAP 60
QY 61 CHANTSMVTHPPATOPQHVONFLYRHCRHFPILLQDVPSKCAQPVFLLVIKSPSNY 120
DB 61 CHANTSMVTHPPATOPQHVONFLYRHCRHFPILLQDVPSKCAQPVFLLVIKSPSNY 120
QY 121 VARRELLRTWGERKVRGQLRLFLYGNASNPHEARKNRLLELAQTHGIIQMDPRD 180
DB 121 VARRELLRTWGERKVRGQLRLFLYGNASNPHEARKNRLLELAQTHGIIQMDPRD 180
QY 181 SFFNLTLLKQVLFLOQETRCANASFVNLGDDVFAHTDNMVFYLDHDPGRILFYGGOLI 240
DB 181 SFFNLTLLKQVLFLOQETRCANASFVNLGDDVFAHTDNMVFYLDHDPGRILFYGGOLI 240
QY 241 NVGPTRAFRSKYYVEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIFPIDVFL 300
DB 241 NVGPTRAFRSKYYVEVVTQNERYPYCGGGFLLSRFTAALRAAHVLDIFPIDVFL 300
QY 301 GKCLELEGKPAHSIGRTSGVRAPSOHSSPDCPFYDILLVHFLPEMLIMMDALNQ 360
DB 301 GKCLELEGKPAHSIGRTSGVRAPSOHSSPDCPFYDILLVHFLPEMLIMMDALNQ 360
QY 361 PMLTCGNQTOIY 372
DB 361 PMLTCGNQTOIY 372

RESULT 2
B3G7_HUMAN STANDARD; PRT; 397 AA.
AC Q9NY97; O9NQ09; O9NQ09; 16-OCT-2001 (Rel. 42, Created)
DT 16-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-1,3-galactosyltransferase 7 (EC 2.4.1.-) (Beta-1,3-galactase 7)
DE (Beta3gal-T7) (b3gal-T7) (UDP-galactose:beta-N-acetylgalucosamine beta-
DE 1,3-galactosyltransferase 7) (UDP-Gal:beta-glcNAc beta-1,3-
DE galactosyltransferase 7) (beta-3-Gx-T7).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Amado M., Carneiro F., Clausen H.;

```

```

RT "Cloning and expression of two beta-1,3-galactosyltransferases:
RT beta3gal-T5 and beta3gal-T6."
RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=urinary bladder;
RT Gromova I., Gromov P., Celis J.E.;
RT "A novel member of beta-1,3-galactosyltransferase family is down
RT regulated during bladder TCC progression."
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Testis;
RX MEDLINE=22386257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Martina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalloe D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Merra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [4]
RP SEQUENCE OF 25-397 FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Oka T., Hayashi K., Sugiyama T., Orenki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimoto K.,
RA Tanai H., Kinata K., Watanabe M., Hirakawa S., Ishi S., Kawai Y.,
RA Saito K., Yamamoto U., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Maeno Y., Kanehori K.;
RT "NEDO human cDNA sequencing project."
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL [5]
RP REVIEW.
RX MEDLINE=20047730; PubMed=10580128;
RA Amado M., Almeida R., Schwientek T., Clausen H.;
RT "Identification and characterization of large galactosyltransferase
RT gene families: galactosyltransferases for all functions."
RL Biochim. Biophys. Acta 1473:35-53(1999).
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId-Q9NY97-1; Sequence=displayed;
CC Name=2;
CC IsoId-Q9NY97-2; Sequence=VSP_001791;
CC Note=No experimental confirmation available;
CC -1- SIMILARITY: Belong to the glycosyltransferase family 31.
CC -1- CAUTION: WAS INDICATED AS B3GAL-T6 IN SUBMITTED DNA ENTRIRS.
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CC -----
DR EMBL; AJ006077; CAB91546.1; -.
DR EMBL; AF288208; AAF97253.1; -.

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DR	EMBL; AF288209; AAF97254.1;	-
DR	EMBL; BC030579; AAH0579.1;	-
DR	EMBL; BC047933; AAA47933.1;	-
DR	EMBL; AK002009; BAA92031.1;	ALT_INIT.
DR	Genew; HGNC:15629; B3GN1.	
DR	GO; GO:0016021; C:integral to membrane; NAS.	
DR	GO; GO:0008495; F:UDP-galactose beta-N-acetylglucosamine beta-	
DR	InterPro; IPR002659; Glyco_trans_11.	
DR	Pfam; PF01762; Galactosyl_Tf_1.	
KW	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;	
KW	Signal-anchor; Golgi stack; Multisome family; Alternative splicing.	
FT	DOMAIN	1 7
FT	TRANSMEM	8 28
FT		(POTENTIAL)
FT	DOMAIN	29 397
FT	CARBOHYD	79 79
FT	CARBOHYD	89 89
FT	CARBOHYD	127 127
FT	CARBOHYD	173 173
FT	CARBOHYD	219 219
FT	VASAPLIC	1 11
FT		/FTID=VSP_001791.
FT	CONFLICT	11 11
FT	SEQUENCE	397 AA; 46022 MW; B104ECCAE26DC4AC CRC64;
SQ		L -> IL (IN REF. 1).
Query Match	30.0%; Score 601; DB 1; Length 397;	
Best Local Similarity	41.3%; Pred. No. 1.5e-45;	
Matches 125; Conservative	51; Mismatches 117; Indels 10; Gaps 5;	
OY	65 TSMWTNHPFAQPQKVNQNFLLRYHRHFPLLODPSPKCAQPVFLLYIKSSPSNYARE	124
Db	103 TSVT--GFNNLPDRFKDFLLYLKRKNYSLLTD-QPDCKAKKPFLLAIKSLTPFARRQ	159
OY	125 LLRTWGRRKKVKGLQLRLFLVGTASNPHBAKKNRLLLEAQTGDILOMDFHSFFN	184
Db	160 AIRSWMGESNAAGNTVVRFVLGGTPTPEBDNHPPDLSDMLKESEKGQDILMMNVADTFN	219
OY	185 LTLKQVLFLOWOETRCANASFYLNCGDDVDVAHTDNMFYLO-DHDGRHLFVGOLIONV	242
Db	220 LSLKEVLLFLRWVSTSCPDTEFEVFKGDVVFNTHIILYNLSISKTKADLFIGDVHNA	279
OY	243 GPIAFWSKYVVEPVYVTOENBRYPRVCGGGGFLSFSTAALRAHVLDIPRIDVFICGM	302
Db	280 GPBHDKKLKYYIVPEV-VSGLYPPVPAAGGGGYSGHLMRLYHTDYQVLYPIDVVYIGM	338
OY	303 CLELEGTLKPASHSGIRTSGVBARPSQHLSFPDCEFRDLLLVHRYFEMLLMWMDLANOPN	362
Db	339 CLQKLGLVPEKHGKERTFDIEBKNN---NICSYVDLMLVNSRKPOEMIDMSLOSAN	394
OY	363 LTC 365	
Db	395 LKC 397	
RESULT 3		
B3G5_GORGO		
ID AC O9N253;	STANDARD;	PRT; 300 AA.
DT 16-OCT-2001 (Rel. 40, Last Created)		
DT 16-OCT-2003 (Rel. 41, Last Annotation Update)		
DT 28-FEB-2003 (Rel. 41, Last Annotation Update)		
DE Beta-1,3-galactosyltransferase 5 (EC 2.4.1.-) (Beta-1,3-GalTase 5)		
DE (BetaGal-T5) (hbGal-T5) (UDP-galactose:beta-N-acetylglucosamine beta-		
DE 1,3-galactosyltransferase 5) (UDP-Gal:beta-glucNAc beta-1,3-		
DE galactosyltransferase 5) (Beta-3-Gx-T5) (Fragment).		
GN B3GAT5.		
OS Gorilla gorilla gorilla (Lowland gorilla).		
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.		
OX NCBI_Taxid=9595;		
RP SEQUENCE FROM N.A.		
RA Liu Y., Saitou N.;		

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RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF GAL TO GLCNAC-BASED ACCEPTORS
CC WITH A PREFERENCE FOR THE CORE 3-O-LINKED GLYCAN
CC GLCNAC(BETA1,3)GALNAC STRUCTURE. CAN USE GLYCOPOLIPID LC3CER AS AN
CC EFFICIENT ACCEPTOR (BY SIMILARITY).
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential) .
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
-----
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-----
CC EMBL; AB041416; BAA94501.1; -.
DR InterPro; IPR002659; Glyco_tran_31.
DR Pfam; PF01762; Galactosyl_T; 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Multimeric family.
FT DOMAIN 1 7
FT TRANSMEM 8 28
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT (POTENTIAL).
FT CATALYTIC (POTENTIAL).
FT LUMENAL (POTENTIAL).
FT DOMAIN 29 >300
FT CARBOHYD 130 130 (POTENTIAL).
FT CARBOHYD 130 130 (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 300 AA; 35104 MW; 1AA11692BDE9F06FA CRC64;

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Query Match	20.7%;	Score 416;	DB 1;	Length 300;
Best Local Similarity	34.0%;	Pred. No. 2,3e-29;		
Matches 100;	Conservative 57;	Mismatches 109;	Indels 28;	Gaps 8;

Qy	73	FATPOHVNQLLRYHCRHFPFLIDVPPSKCAQ-PVELLVIKSSPSNVYRRELLRRTWG	131
Db	26	YSLNPFKEQSF-VYKKQGNFLKL---PDTQCRQPPFLVLTVSSHQQLAERMAIRQTWG	81
Qy	132	KERVNRGLQRLFLVLTASNPHHAKRVNLLLELAQTHDDIIQMDHDSFNNLTQVL	191
Db	82	KERVNVKQKLTFFPLIDGTTSSAAETKEVDQ---ESGRHDDIIQKDLVDVYNNLTQTM	137
Qy	192	FLQWQETRCNANASVLVNGDDVFAHTNNMFYLQDHPGRLFLFGQLIQNVGPIRAFWSK	251
Db	138	GIEVWHFPCQQAAMVMTDSDMFINDVLTVELLKKRTRFRFLGKLNEFPTRQFSK	197
Qy	252	YVVEVATONERYPPYGGGGFLSRLPTAALRRAAHVLDIPIDVFLGMCLE----	306
Db	198	WFWKSEYPMWRYPFCSTGTGYVFSGDVAQVNVVSKSVYIKLEDFVFGCLERLIRL	257
Qy	307	EGL--KRASHSGIRTSQVRAPSQHLSSFQDFCRDLLVVRFLPYELLMWMDL	358
Db	258	ELHLSQTFPPFG-----GLR-----FSVCLFRIRIVACHPIKRTLLDYQAL	299

RESULT 4				
B3G5_HUMAN				
ID	B3G5_HUMAN	STANDARD;	PRT;	310 AA.
AC	Q9Y2C3; Q9NY96; Q9P1X6; Q9P1X7;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Beta-1,3-galactosyltransferase 5 (EC 2.4.1.-)			
DE	(Beta3Gal-T5) (B3Gal-T5) (UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase 5) (UDP-Gal:beta-GlcNAc beta-1,3-galactosyltransferase 5) (Beta-3-Gx-T5).			
DE	B3GALT5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Colorectal adenocarcinoma;
RX MEDLINE=99230269; PubMed=10212226;
RA Ieshiki S., Togayachi A., Kudo T.,
RA Kubota T., Kicajima M., Shiraihi N., Sasaki K., Andoh T.,
RA Narimaru H.;
RT "Cloning, expression and characterization of a novel UDP-
RT galactose:beta-N-acetylglucosamine betal,3-galactosyltransferase
RT (betagal-T5) responsible for synthesis of type I chain in colorectal
RT and pancreatic epithelia and tumor cells derived therefrom.";
RL J. Biol. Chem. 274:12499-12507(1999).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99337698; PubMed=10406968;
RA Zhou D., Berger E.G., Hennes T.;
RT "Molecular cloning of a human UDP-galactose:GLCNACbetal,3GALNAC
RT betal, 3 galactosyltransferase gene encoding an O-linked
RT core3-elongation enzyme.";
RL Eur. J. Biochem. 263:571-576(1999).
RN
RP SEQUENCE FROM N.A.
RX Amado M., Carneiro F., Clausen H.;
RT "Cloning and expression of two beta-1,3-galactosyltransferases:
RT betagal-T5 and betagal-T6.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Iehi K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kuch J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordstok G., Hornischer K., Brandt P.,
RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramer J., Beck A., Klages S., Hennig S., Riesemann L., Dagand E.,
RA Wehnemeyer S., Borzym K., Gardiner K., Nizetic D., Francis P.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN
RP SEQUENCE OF 1-298 FROM N.A.
RA Liu Y., Salton N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN
RP REVIEW.
RX MEDLINE=20047730; PubMed=10580128;
RT Amado M., Almeida R., Schwientek T., Clausen H.;
RT "Identification and characterization of large galactosyltransferase
RT gene families: galactosyltransferases for all functions.";
RL Biochim. Biophys. Acta 1473:35-53(1999).
CC
CC -1- FUNCTION: CATALYZES THE TRANSFER OF GAL TO GLCNAC-BASED ACCEPTORS
CC WITH A PREFERENCE FOR THE CORE3 O-LINKED
CC GLCNAC(BETA1,3)GALNAC STRUCTURE. CAN USE GLYCOLIPID LIGAND AS AN
CC EFFICIENT ACCEPTOR.
CC
CC -1- PATHWAY: Glycosylation.
CC
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
CC
CC -1- TISSUE SPECIFICITY: EXPRESSED IN STOMACH, JEJUNUM, COLON,
CC PANCREAS, SMALL INTESTINE, TESTIS AND GASTROINTESTINAL AND
CC PANCREATIC CANCER CELL LINES. HARDLY DETECTED IN LUNG, LIVER,
CC ADRENAL GLAND AND PERIPHERAL BLOOD LEUKOCYTES.
CC
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
CC
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CC
DR EMBL; AB020337; BAA77664.1; -
DR EMBL; AF145794; AAF07880.1; -
DR EMBL; AJ006078; CAB91547.1; -
DR EMBL; AL163280; CAB90446.1; -
DR EMBL; AB041412; BAA94497.1; -
DR EMBL; AB041413; BAA94498.1; -
DR GenBank; HGNC:920; B3GALT5.
DR MIM; 604066; -
DR GO; GO:0008499; F:UDP-galactose beta-N-acetylglucosamine beta. . .; TAS.
DR GO; GO:0006486; P:protein amino acid glycosylation; TAS.
DR InterPro; IPR002659; Glyco_trans_31.
DR Pfam; PF01762; Galactosyl_T; 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Multigene family.
FT DOMAIN 1 7
FT TRANSMEM 8 28
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 29 310
FT LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 F -> Y (IN REF. 3).
FT CONFLICT 23 23 Y -> N (IN REF. 3).
FT CONFLICT 26 26 G -> V (IN REF. 5; BAA94497).
FT CONFLICT 42 42 M -> T (IN REF. 3 AND 5; BAA94497).
FT CONFLICT 85 85 O -> R (IN REF. 5; BAA94497).
FT CONFLICT 114 114 K -> E (IN REF. 5; BAA94497).
FT CONFLICT 234 234 L -> R (IN REF. 5; BAA94497).
FT CONFLICT 277 277 LDYWO -> WTIGR (IN REF. 5; BAA94498).
FT CONFLICT 293 297
SQ SEQUENCE 310 AA; 36189 MW; 4DD7A19E3E648AA9 CRC64;

Query Match 20.7%; Score 416; DB 1; Length 310;

Best Local Similarity 34.0%; Pred. No. 2,4e-29; Matches 100; Conservative 57; Mismatches 109; Indels 28; Gaps 8;

QY 73 FATPOHVNFLYHCHHFPFLLODPSPKCAQ-PVFLILVYKSSPSSVYRREILRTWG 131
DB 26 YLNFKEQSF-VYKQDNFLTL--PDTDCQRPFLVLVTSSHKOLAEMAIROQWG 81
QY 132 RRRKRGQLRLPLVGVASNDHAKKRNRLLEAOHGDLOQDFDPSFRLTLKQVL 191
DB 82 KRRVKGKQLKTFLLGTSSAETKEVDQ----ESORHGDILQDFDVLVYNNLTKTMM 137
QY 192 FLOWETRCANASPVINGDDVFAHTDNMVFYLODHDGRHLFVQOLIQNVGPPIAFMSK 251
DB 138 GIEWHRCPCQAAPFVKTDSDMFIVNDVLTLLKXNRTTFETGFLKINERPIIQPSK 197
QY 252 YVPEVVTQNERYPYCGGGFLSRFTAALRRAAHVLDIFPDVFLGMLF-----L 306
DB 198 WVSSEVPMWDRYPFGCGTGVFSGDVAAGVYNSKSVPIKLEDDVFGCLERLNTRL 257
QY 307 EEL--KPSHSGIRKISGVRAEQHLSFDPCCYRDLVLVHRLPYEMLLMQDAL 358
DB 258 EELHSPQTFPFPG---GLR-----PSVCLFRRIVACHFIKPTLLDYQWAL 299

RESULT 5

B3G5_PANPA
ID B3G5_PANPA STANDARD; PRT; 301 AA.
AC Q9N294;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE beta-1,3-galactosyltransferase 5 (EC 2.4.1.1-) (Beta-1,3-GalTase 5)
DE (Beta3Gal-T5) (b3gal-T5) (UDP-galactose:beta-N-acetylglucosamine beta-
DE 1,3-galactosyltransferase 5) (UDP-Gal:beta-GlcNAc beta-1,3-
DE galactosyltransferase 5) (beta-3-Gx-T5) (Fragment).
GN B3GALT5.
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_Taxid=9597;

```
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Salton N.;
RU Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF GAL TO GLCNAC-BASED ACCEPTORS
CC WITH A PREFERENCE FOR THE CORE3 O-LINKED GLYCAN
CC GLCNAC(BETA1,3)GALNAC STRUCTURE. CAN USE GLYCOLIPID LC3CER AS AN
CC EFFICIENT ACCEPTOR (BY SIMILARITY).
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB041415; BAA94500.1; -.
DR InterPro: IPR002659; Glyco_crange_31.
DR Pfam: PF01762; Galactosyl_T; 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Multigene family.
FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 8 28 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 1 7 (POTENTIAL).
FT FT LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 301 301
SQ SEQUENCE 301 AA; 35222 MW; E04CC70F41CB29FD CRC64;

Query Match 20.6%; Score 413; DB 1; Length 301;
Best Local Similarity 34.9%; Pred. No. 4.3e-29;
Matches 94; Conservative 52; Mismatches 99; Indels 24; Gaps 6;

QY 98 VPSKCAQ-PVFLILYKSSPSNYVRRELLRRTWGRERKRGQLRLFLVGTASNPHEA 156
DB 47 LPDTRQRPPLFVLVLTSSHQLAERMAIRQTMGKERKRYGQLTKTFILGTTSSAERT 106
QY 157 RKYNRLLEAQTGDIQWDFHDSFENLTQKQVLFQWQETRCANASPVYNGDDVFAH 216
DB 107 KEVDQ---ESQRHGDIQKDFLDVYNNLTQKTMGIEWVHRPCPOAFAFMKTDSDMFIN 162
QY 217 TDNMVYFLQDHDGRHLFVGQLIQNVGPIRAFWSKYVPEVTQNERYPYCGGGFLLS 276
DB 163 VDLTTELLKKNNTTFFGFLKLNFRIPQPSKMFVSKSEYPMWRYPFGSGTGVFS 222
QY 277 RFTAALRAAAVLDLFFPIDVFLGMCLE-----LEGL-KPASHSGIRTSQVRAQSOL 329
DB 223 GDVASQVYVNSSEVPYIKLBDVFGCLERLNIRLELSQPIFFPG-----GLR----- 272
QY 330 SSFDPGCFYRDLLVHRFLPYEMLLMWDL 358
DB 273 --FVCRFRRIYVACHFIKPRTLDDYWQAL 299

RESULT 6
B3G5_PANTR STANDARD; PRT; 297 AA.
ID B3G5_PANTR
AC Q9N255;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-1,3-galactosyltransferase 5 (EC 2.4.1.-) (Beta-1,3-GalTase 5)
DE (Beta3Gal-T5) (b3Gal-T5) (UDP-galactose:beta-N-acetylglucosamine beta-
DE 1,3-galactosyltransferase 5) (UDP-Gal:beta-Gal:beta-GlcNAc beta-1,3-
DE galactosyltransferase 5) (Beta-1-Gx-T5) (Fragment).
GN B3GALT5.
OS Pan troglodytes (Chimpanzee).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Salton N.;
RU Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF GAL TO GLCNAC-BASED ACCEPTORS
CC WITH A PREFERENCE FOR THE CORE3 O-LINKED GLYCAN
CC GLCNAC(BETA1,3)GALNAC STRUCTURE. CAN USE GLYCOLIPID LC3CER AS AN
CC EFFICIENT ACCEPTOR (BY SIMILARITY).
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB041414; BAA94499.1; -.
DR InterPro: IPR002659; Glyco_crange_31.
DR Pfam: PF01762; Galactosyl_T; 1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Multigene family.
FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 8 28 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 1 7 (POTENTIAL).
FT FT LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 297 297
SQ SEQUENCE 297 AA; 34850 MW; BB7963250A837A28 CRC64;

Query Match 20.0%; Score 402; DB 1; Length 297;
Best Local Similarity 34.6%; Pred. No. 4e-28;
Matches 92; Conservative 52; Mismatches 98; Indels 24; Gaps 6;

QY 98 VPSKCAQ-PVFLILYKSSPSNYVRRELLRRTWGRERKRGQLRLFLVGTASNPHEA 156
DB 47 LPDTRQRPPLFVLVLTSSHQLAERMAIRQTMGKERKRYGQLTKTFILGTTSSAERT 106
QY 157 RKYNRLLEAQTGDIQWDFHDSFENLTQKQVLFQWQETRCANASPVYNGDDVFAH 216
DB 107 KEVDQ---ESQRHGDIQKDFLDVYNNLTQKTMGIEWVHRPCPOAFAFMKTDSDMFIN 162
QY 217 TDNMVYFLQDHDGRHLFVGQLIQNVGPIRAFWSKYVPEVTQNERYPYCGGGFLLS 276
DB 163 VDLTTELLKKNNTTFFGFLKLNFRIPQPSKMFVSKSEYPMWRYPFGSGTGVFS 222
QY 277 RFTAALRAAAVLDLFFPIDVFLGMCLE-----LEGL-KPASHSGIRTSQVRAQSOL 329
DB 223 GDVASQVYVNSSEVPYIKLBDVFGCLERLNIRLELSQPIFFPG-----GLR----- 272
QY 330 SSFDPGCFYRDLLVHRFLPYEMLLMW 355
DB 273 --FVCRFRRIYVACHFIKPRTLDDYW 296

RESULT 7
B3G5_MOUSE STANDARD; PRT; 308 AA.
ID B3G5_MOUSE
AC Q9J167;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta-1,3-galactosyltransferase 5 (EC 2.4.1.-) (Beta-1,3-GalTase 5)
DE (Beta3Gal-T5) (b3Gal-T5) (UDP-galactose:beta-N-acetylglucosamine beta-
DE 1,3-galactosyltransferase 5) (UDP-Gal:beta-GlcNAc beta-1,3-
```


RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasle F.,
RA	Dachbender L., Marsina K., Farmer A.R., Rubin G.W., Hong L.
RA	Stepleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Ueda N.B., Tohyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano L.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA	Vallian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Jackson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywiński M.J., Skala U., Smallov D.E.,
RA	Schmeh A., Schen J.E., Jones S.J.M., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length
RL	human and mouse cDNA sequences."
CC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-1- FUNCTION: Involved in GM1/GM2/GAL ganglioside biosynthesis.
CC	-1- CATALYTIC ACTIVITY: UDP-galactose + N-acetyl-D-glucosamine]-(N-
CC	acetylneuraminyl)-D-galactosyl-D-glucosyl-N-acetylphingosine = UDP
CC	+ D-galactosyl-D-N-acetyl-D-galactosaminyl-(N-acetylneuraminyl)-D-
CC	galactosyl-D-galactosyl-N-acetylphingosine.
CC	-1- PATHWAY: Glycosylation.
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi.
CC	-1- TISSUE SPECIFICITY: Highly expressed in heart, skeletal muscle and
CC	pancreas and, to a lesser extent, in brain, placenta, kidney,
CC	liver and lung.
CC	-1- SIMILARITY: Belongs to the glycosyltransferase family 31.
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb.ch/announce
CC	or send an email to license@isb.ch).
DR	EMBL; Y15061; CAH7345.1; -
DR	EMBL; AL031228; CAA20330.1; -
DR	EMBL; AB026730; BAA88988.1; -
DR	EMBL; BC032574; AAH32574.1; -
DR	GeneW; HGNC:919; BGALTL4.
DR	MIM; 603095; -
DR	GO; GO:0008499; F:UDP-galactose beta-N-acetylglucosamine beta. .; TAS.
DR	GO; GO:0006486; P:protein amino acid glycosylation; TAS.
DR	InferPro; IPRO02659; Glyco_trans_31.
DR	Pfam; PF01762; Galactosyl_T; 1.
KW	Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW	Signal-anchor; Golgi stack.
FT	DOMAIN
FT	TRANSMEM
FT	1 19
FT	1 8
FT	CYTOPLASMIC (POTENTIAL) .
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT	(POTENTIAL) .
FT	LUMENAL, CATALYTIC (POTENTIAL) .
FT	CARBHYD 149 149 N-LINKED (GLCNAc. .) (POTENTIAL) .
SO	SEQUENCE 378 AA; 41536 MW; 4B5DFC72AE96213 CRG64;
Query Match	15.6%; Score 312; DB 1; Length 378;
Best Local Similarity	29.9%; Pred. No. 4.8e-20;
Matches 84; Conservative	43; Mismatches 116; Indels 38; Gaps 6
Oy	106 PVLLVLYKSSPSNYRRELRRTWGGRKKVGLQLRLFLVTGSNDPEHA-RKVNRLLLE 1644
Db	70 PPFLVLCTAPENLNQNRNIRASWGLREARGLVQTLFLTGSENAQHPRWSQSGSDLA 1529
Oy	165 LEAQTGSDILOMFHSFNLTKQYLFLQMERTCANASFNLDDDVFAHTDMNFYLL 2244
Db	130 SESAAQGDIIQAAPFODSYRNLTLLKTLSGLMAEKRCPMARYLLAKTDVVYNNVELSEL 1899
Oy	225 -----QDHDEGRH-----LFVGOLIQNGPIRFATFSKYYPREV 2571
Db	190 VLRGRHWQWERSTEQREADEGGCVHLSEVPFLLYIGRVAMRNRPRTGCGHRASEE 2494
Oy	258 VTONE-RVPPYCGGGGFLSRFTAALRRAAHVLDIFPIDVFLMGCLDLGLKPASHS 3155

[illegible]

Qy	100	PSKC---AQVFLVLVTKSSPSNVRRRELLARTWGRKKVQLRLFLVTASNPHEA	156
Db	61	POACGGSGPPFLILITCTAPRPHLNQNNATIRGSGAIREARGRVQTLFLTSGMQQA	120
Qy	157	RKVNRLLELEAQTGDLTQNDPFDSPFNLTLLKQVLFQWQETFCANSPFLNDDVFAH	216
Db	121	D-----LASSAAQGDVLQASFDQSYKNLTILKTILTGLNWNKKCPMARVTLKTDVVYN	175
Qy	217	TDMNVFYL-----QDHPGRH-----LFVGQLIQNVPRAFWMS	250
Db	176	VPFLVSELIRGGRPSSEQWQKGEPOEETTAIVHEHKKQAVPLIYLGVHWRVAPTRPES	235
Qy	251	KYYVPEVWQNE--RYRPPYCGGGGFLILSRSTAALRAAHVLDIFPIDVFLGMCLEEG	308
Db	236	RHHVSELMPEWNGPPPPYASGTGVYLSISAVOLLTKVSRADYLPLEDVFSVARRVG	295
Qy	309	LKPASHSGIRTSGVRAPSOHLSSFPDPCFYRDLIVHRFLPYEMLLMMDALQNPILTCGNQ	368
Db	296	LAP-THC-VKLAG----ATHYPLDRCCYCGKFLITSHKVPDWKMQEAMKVLGRGIN--GRR	346
Qy	369	TQ 370	
Db	347	TE 348	
RESULT 10			
ID	B3G4	MOUSE	
AC	Q9Z0F0; Q91VC1; Q9Z0T8; Q9Z0U9;	STANDARD; PRT; 371 AA.	
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Beta-1,3-galactosyltransferase 4 (BC 2.4.1.62) (Beta-1,3-gal-4)		
DE	Beta3Gal-T4 (b3gal-T4) (Ganglioside galactosyltransferase) (UDP-		
DE	galactose:beta-N-acetyl-galactosamine-beta-1,3-galactosyltransferase)		
GN	B3GALT4.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL		
RC	STAGE.		
RC	TISSUE=Fetal;		
RX	MEDLINE=99432136; PubMed=10502288;		
RA	Daniotti J.L., Martina J.A., Zurita A.R., Maccioni H.J.F.;		
RT	"Mouse beta 1,3-galactosyltransferase (Gal/GM1/GD1b synthase): protein		
RT	characterization, tissue expression, and developmental regulation in		
RT	neural retina.";		
RL	J. Neurosci. Res. 58:318-327 (1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129/SvJ;		
RC	Nut/Msf, gmf2, and SWN/Msf;		
RA	Liu Y., Kitano T., Koide T., Shirotshi T., Moriaki K., Saitou N.;		
RT	"Conspicuous differences among gene genealogies of 21 nuclear genes of		
RT	five Mus musculus subspecies.";		
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Involved in GM1/GD1b/Gal ganglioside biosynthesis.		
CC	CATALYTIC ACTIVITY: UDP-galactose + N-acetyl-D-galactosaminyl-(N-		
CC	-acetylneuraminyl)-D-galactose1-D-glucose1-N-acylsphingosine = UDP		
CC	+ D-galactosyl-N-acetyl-D-galactosaminyl-(N-acetylneuraminyl)-D-		
CC	galactosyl-D-glucose1-N-acylsphingosine.		
CC	-1- PATHWAY: Glycosylation.		

```

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi.
CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, kidney,
CC lung and testis.
CC -1- DEVELOPMENTAL STAGE: First expressed at embryonic day 3.
CC Maintained at high levels between days 4 and 7 and declines
CC thereafter to stabilize at low levels after day 10.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
CC
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CC
DR EMBL; AF110520; AAC97977.1; -
DR EMBL; AF082504; AAC69622.1; -
DR EMBL; AF100956; AAC69897.1; -
DR EMBL; AB039164; BAB68688.1; -
DR EMBL; AB039165; BAB68689.1; -
DR EMBL; AB039167; BAB68691.1; -
DR EMBL; AB039168; BAB68692.1; -
DR EMBL; AB039170; BAB68694.1; -
DR EMBL; AB039171; BAB68695.1; -
DR EMBL; AB039172; BAB68696.1; -
DR EMBL; AB039169; BAB68693.1; -
DR EMBL; AB039166; BAB68690.1; -
DR MGD; MGI:1859517; B3gal14.
DR InterPro; IPR002659; Glyco_trans_31.
DR Pfam; PF01762; Galactosyl_T_1.
KW Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Signal-anchor; Golgi stack; Polymorphism.
FT DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 5 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT FT 26 371 LUMENAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 248 248 W -> R (IN STRAIN PGN2).
FT VARIANT 344 344 G -> W (IN STRAIN B1G2/MSF).
SQ SEQUENCE 371 AA; 41235 MW; 323A7EFA56B723B3 CMC64;
Query Match 14.9%; Score 298; DB 1; Length 371;
Best Local Similarity 28.1%; Pred. No. 8.1e-19;
Matches 82; Conservative 55; Mismatches 113; Indels 42; Gaps 9;
QY 106 PVEILLIVKSSPSNVVRELLRTGTGRGRKYRGQLRLPLVGTASNPHEARKYRRLLEL 165
Db 70 PEFLLIVCTAPRHLNQNMALIRASGAIKREKGRVOTLLFG--KPRROQLAD--LSS 124
QY 166 EAQTHGILLQWDFHDSFNNILTKQVLFLOWQETRCANASFYLANGDDVDVFAHTDMMVFL- 224
Db 125 ESAARHDILOASFODSYENLTLLKTLGLINWYKRCPMARYILTKDDDDVYVNPPELVELI 184
QY 225 -----QHDHPRH-----LFVQGLQNGPITAFMSKYVPEVVT 259
Db 185 QRGGESEQWQKGAQOETTAIHEEHRRGQAVPLLYIGRVMHRRAPFTPTPSRHHSVEL 244
QY 260 QNE--RYVPYCGGGGFLISRTFAALARRAAVLDIPIDVFLQMCLEGLKPKASHGI 317
Db 245 PENMGPFPFVASGIVGLSISAVGLILIKVASRAPEPLDEDVFGVSAARRGLAP--THC-V 302
QY 318 RTSGVRAASQHLSSFDPCFTFRDILLVHFLPYEKLMLWMDLANQNLTCGNQOT 369
Db 303 KLAG---ATHYPLDRCCYGFLLTSHKVDPMWQOEMAKLVSGMN--GERT 347

```


DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-export membrane protein secD.
GN secD OR RV2587C OR MT2664 OR MTCY227.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv.
RX MEDLINE=96295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gae S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Dajels K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Javels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
RA Sultson J.E., Taylor K., Whitehead S., Barrall B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M., Hatt D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Ustebach T., Weidman J., Kouri H., Gill J., Mikula A.,
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
CC -1- FUNCTION: Involved in protein export.
CC -1- SUBUNIT: Part of the prokaryotic protein translocation apparatus
CC which comprises secA, secB, secD, secE, secF, secG and secY (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the secD/secE family. SecD family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z77724; CAB01256.1; -
DR EMBL: AE007100; AAK46977.1; ALT_INIT.
DR PIR: B70726; B70726.
DR TIGR: MT2664; -
DR Tuberculae; RV2587C; -
DR InterPro: IPR005791; SecD.
DR InterPro: IPR003335; SecD_secF.
DR Pfam: PF02355; SecD_secF. 1.
DR TIGRFAMs: TIGR009167.2A0604s01. 1.
DR TIGRFAMs: TIGR01129; secD. 1.
KM Protein transport; Translocation; Transmembrane; Membrane;
KW Complete proteome.
FT TRANSMEM 13 POTENTIAL.
FT TRANSMEM 385 405 POTENTIAL.
FT TRANSMEM 410 430 POTENTIAL.
FT TRANSMEM 441 461 POTENTIAL.
FT TRANSMEM 489 509 POTENTIAL.
FT TRANSMEM 514 534 POTENTIAL.
SQ SEQUENCE 573 AA; 60267 MW; 5A8F42E2C0389CE2 CRC64;
Query March 6.4k; Score 129; DB 1; Length 573;
Best Local Similarity 22.2k; Pred. No. 0.0012;
Matches 88; Conservative 40; Mismatches 114; Indels 154; Gaps 18

Oy	22	LLLFSLFSLVBPRTKVOECPRAIPRLALMPRTPTRRAPRSCANTSMWTHPDEFAPOHVO	81
Dd	116	LYIRPLVINSMPRAAPAEFQPARPS--AEPQPPGQRA-APRAAGGAPARSPQAGQPR---	165
Oy	82	NFLLYHCRHFPLLQDPVPS-----KCAQVFLLLVTKSSPSNVYRELLRTWGR	132
Dd	170	-----PYQDPAPSPNPPTSPAPSPAPRA-----EAPATDPRKDLAERI-AQ	210
Oy	133	ERKVRGLQRLPLVGTASNPHEAKVRRLLELEQTHGDILOMDPHDSFPNLTUKQVL	199
Dd	211	EKKLR-----OSTAQYQWMA-----	226
Oy	193	LQWQETRCANASFVLNGDD-----VPAHTDNMVFYLODHPGRHLLFVGOLIQNV-----	242
Dd	227	LQFQAIRC-ESDDIILAGNDPKLPLVGTSTDBHKRAYLL-----ASIIISGQIQNATSGMD	287
Oy	243	-----GPIRAFMSKRYVPEVVTO-----NERYPYCGGGGFL	274
Dd	282	QRGIGYVVDLQFGKPAANIWADYTAAHIGTQAFPLDSQVSAPOIQEAPR-----GGRTQ	337
Oy	275	LS-----RFTPAALRRRAHY-----LDIFPDDVFLGMCLEGLKPAHSIGRTSGVR	323
Dd	338	ISGGDPPFPAAATARQALANVLKYGSLPLSFPESEAOYASATIGLSLR-----AGMT	368
Oy	324	APSOHLSSFDPCFYRDLILVHRFLPYEMULIMWDALN	359
Dd	389	AGAIQILL-----LVVYVSLLYRRVDIGLITLALS	415

ID	REFNG	HUMAN	STANDARD	PRT	331 AA.
AC	09y644	000588			
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Beta-1,3-N-acetylglucosaminyltransferase radical fringe (EC 2.4.1.222)				
DE	(O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase).				
GN	RFNG.				
OS	Homo sapiens (Human).				
OC	Bukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE OF 141-331 FROM N.A.				
RX	MEDLINE=97330691; Pubmed=9187150;				
RA	Johnson S.H., Rauekolb C., Wilson R., Prabhakaran B., Irvine K.D.,				
RA	Vogt T.F.,				
RT	"A family of mammalian fringe genes implicated in boundary				
RT	determination and the Notch pathway."				
RL	Development 124:2245-2254(1997).				
RN	[2]				
RP	SEQUENCE OF 1-191 FROM N.A.				
RX	MEDLINE=99272806; Pubmed=10341080;				
RA	Moran J.L., Johnston S.H., Rauekolb C., Bhalerao J., Bowcock A.M.,				
RA	Vogt T.F.,				
RT	"Genomic structure, mapping, and expression analysis of the mammalian				
RT	Lumatic, Mantic, and Radical fringe genes."				
RL	Mamm. Genome 10:535-541(1999).				
CC	-1- FUNCTION: Glycosyltransferase that initiates the elongation of O-				
CC	linked fucose residues attached to EGF-like repeats in the				
CC	extracellular domain of Notch molecules. May be involved in limb				
CC	formation and in neurogenesis (by similarity).				
CC	-1- CATALYTIC ACTIVITY: Transfers a beta-D-GlcNAc residue from UDP-D-				
CC	GlcNAc to the fucose residue of a fucosylated protein acceptor.				
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).				
CC	-1- SIMILARITY: Belongs to the glycosyltransferase family 31.				
CC	-----				
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RT determination and the Notch pathway." ;
 RL Development 124:2245-2254(1997).
 [6]
 RP SIMILARITY WITH LEXI FAMILY.
 RX MEDLINE=97148682; PubMed=9019410;
 RA Yuan Y.P., Schultz J., Miodzik W., Bork P.;
 RT "Secreted fringe-like signaling molecules may be
 RL glycosyltransferases." ;
 RN Cell 88:9-11(1997).
 [7]
 RP CHARACTERIZATION.
 RX MEDLINE=20388659; PubMed=10935626;
 RA Moloney D.J., Panh V.M., Johnston S.H., Chen J., Shao L., Wilson R.,
 Wang Y., Stanley P., Irvine K.D., Haltiwanger R.S., Vogt T.F.;
 RT "Fringe is a glycosyltransferase that modifies Notch." ;
 RL Nature 406:369-375(2000).
 [8]
 RP CHARACTERIZATION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF ASP-236.
 RX MEDLINE=20359806; PubMed=10899003;
 RA Munro S., Freeman M.;
 RT "The notch signaling regulator fringe acts in the Golgi apparatus and
 RL requires the glycosyltransferase signature motif DXD." ;
 RN Curr. Biol. 10:813-820(2000).
 [9]
 RP CHARACTERIZATION.
 RX MEDLINE=20439513; PubMed=10965380;
 RA Blair S.S.;
 RT "Notch signaling: Fringe really is a glycosyltransferase." ;
 RN Curr. Biol. 10:R608-R612(2000).
 CC -1- FUNCTION: Glycosyltransferase involved in the elongation of O-
 CC linked ligands to activate notch signaling. Possesses fucose-
 CC specific beta-1,3-N-acetylglucosaminyltransferase activity.
 CC Boundary-specific cell-signaling molecule that is responsible for
 CC dorsal-ventral cell interactions during wing development.
 CC CATALYTIC ACTIVITY: Transfers a beta-D-GlcNAc residue from UDP-D-
 CC GlcNAc to the fucose residue of a fucosylated protein acceptor.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Golgi.
 CC -1- TISSUE SPECIFICITY: Expressed in dorsal cells.
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 31.
 CC
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 CC
 CC EMBL: L35770; AAA64525.1; -;
 CC EMBL: AE003592; AAF51658.2; -;
 CC EMBL: AY070927; AAL48549.1; -;
 CC PIR: A55376; A55376.
 CC FLYBASE: FBgn0011591; fng.
 CC DR GO: GO:0005783; C:Endoplasmic reticulum; IDA.
 CC DR GO: GO:0005795; C:Golgi stack; IDA.
 CC DR GO: GO:0016757; F:transferase activity, transferring glycosyl. . . ; IMP.
 CC DR GO: GO:0008194; F:UDP-glycosyltransferase activity; IDA.
 CC DR GO: GO:0007450; F:dorsal/ventral pattern formation, imaginal. . . ; IDA.
 CC DR GO: GO:0007933; P:egg chamber formation (sensu Insecta); IMP.
 CC DR GO: GO:0007456; P:eye morphogenesis (sensu Drosophila); IDA.
 CC DR GO: GO:0007478; P:leg disc metamorphosis; IDA.
 CC DR GO: GO:0008593; P:regulation of N signaling pathway; IMP.
 CC DR GO: GO:0008587; P:wing margin morphogenesis; IMP.
 CC DR InterPro: IPR003378; Fringe.
 CC DR Pfam: PF02434; Fringe; 1.
 CC KW Developmental protein; Transferase; Glycosyltransferase;
 CC Transmembrane; Signal-anchor; Golgi stack.
 CC FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 35 412 LUMENAL (POTENTIAL).
 CC FT MUTAGEN 236 236 D->A: ACTIVITY ABOLISHED.
 CC SQ SEQUENCE 412 AA; 46992 MW; 0B1D3EFC4B7668 CRC64;

Query Match 4.8%; Score 95.5; DB 1; Length 412;
 Best Local Similarity 19.4%; Pred. No. 0.71;
 Matches 73; Conservative 56; Mismatches 120; Indels 127; Gaps 18;
 QY 5 RHRRPNTLLIAGA--FTLLLSLVSPPTCKVQEOPPAIPALA----- 48
 DB 12 RFRRIQAMMLAVAVVMTLLYQSAVGYGIVQ---PISQVDAALSAVTHRDQLD 68
 QY 49 --WPTPTRP-AAPCHANTSMYTHPDF-----ATQPOVQNFLLYRCHRPPL 95
 DB 69 YVQSTPTQAGAPAPASPTVIIRDIRSFNSDIEVSRPATTLLTELRARSNGEL 128
 QY 96 QDV-----PSKCAQVFLILYIKSPSNY--VREELLRFTWGRKRGLOL-- 141
 DB 129 RDISQRAVATPPPPVTELDITISV---KTKQVYDTRALALIKTV-----POLAR 177
 QY 142 -RLFLVGTASNPHEARKVRLLELEAQTGHDILQWDFHDSF-FNLTAKVLFLOQETR 199
 DB 178 DQTFPFDTDDHYQEKTKGHLINTKCS-----QGHFRALCCKMSAELDVLE----- 226
 QY 200 CANASFLVNGDDVFAHTDMVFLYLDQHDGRLFPVGLQVNGVIRAFSKTYVEV-- 257
 DB 227 -SGKQWCFHPDDNNVYVPRVLVLDLDEYSPSDVWYLGK-----PSISS 268
 QY 258 -----VTQNEHYPPY--CGGGGFLSRFTALARRAAVLDIFPI----- 295
 DB 269 PLEIHLDKNTTNNKITTFFATGAGFCLSR-----ALTLKMLPIAGGKRFISG 319
 QY 296 -----DDVFLGMCLE 305
 DB 320 DKIRPDDVYMGFTIE 335
 RESULT 14
 ID POOF KLEPN STANDARD; PRT; 761 AA.
 AC P27508;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthetase protein P (BC 3.4.99.-) (Pyrroloquinoline
 GN quinine biosynthesis protein P).
 OS POOF.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 418;
 RX MEDLINE=92212293; PubMed=1313537;
 RA Meulenber J.J.M., Sellink E., Riegmans N.H., Postema P.W.;
 RT "Nucleotide sequence and structure of the Klebsiella pneumoniae pqq
 RT operon." ;
 RL Mol. Gen. Genet. 232:284-294(1992).
 CC -1- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
 CC biosynthesis. It is thought that this protein is a protease that
 CC cleaves peptides bond in a small peptide (gene PQA), providing
 CC the glutamate and tyrosine residues which are necessary for the
 CC synthesis of PQQ.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -1- SIMILARITY: Belongs to peptidase family M6.
 CC
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DR EMBL: X58778; CAA41584.1; -.
DR PIR: S20458; S20458.
DR MEROPS; M16.006; .
DR InterPro; IPR001431; Peptidase_M16.
DR InterPro; IPR007863; Peptidase_M16_C.
DR Pfam; PF00675; Peptidase_M16; 1.
DR Pfam; PF05193; Peptidase_M16_C; 1.
DR PROSITE; PS00143; INSULINASE; 1.
DR PQQ biosynthesis; Hydrolase; Metalloprotease; Zinc.
FT METAL 49 49 ZINC (BY SIMILARITY).
FT ACT_SITE 52 52 BY SIMILARITY.
FT METAL 53 53 ZINC (BY SIMILARITY).
FT METAL 130 130 ZINC (BY SIMILARITY).
SQ SEQUENCE 761 AA; 83616 MW; 1871820BC8E39B5 CRC64;

Query Match 4.8%; Score 95.5; DB 1; Length 761;
Best Local Similarity 23.5%; Pred. No. 1.6; Mismatches 64; Indels 99; Gaps 11;
Matches 55; Conservative 16;

7 RRPNATLILAIAGFTLLFSLVSPCTKVQEQPAPLPEALA----- 48
505 RRPREALQAIIRQLAPVASTLTPSPESIAIRHLMQLPRLGTSGHOKMTALAGSAE 564
49 ---W-----PPTPRPAPAPCHAMTSWVTHPD-----FATOPQHYQNF--- 85
565 DAQWVARQSLITAPNPMPAPAPCRGVERLVFGSDTALLVFLPLPDGASLAAARLL 624
86 YRCHRFPLLDVVPSCAQPVFL-----LVYKSSPSNY 120
625 AQHC-----EPLFQRLRVQEQIGYVVSQYQVADRDILMALQSPD-- 667
121 VRR--ELRRTWGR-----ERKVRGLQRLFLVGTASNPHKAKVRL 162
668 -RRAGEILRR--CGKDFLRQLAPMDEATFRPLQQLAAQI-RASRPEARALSHL 717

RESULT 15
DPOL_HPBVA STANDARD; PRT; 832 AA.
AC P24024;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE P protein [includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
GN Hepatitis B virus (strain alpha1).
OS Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10411;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90266476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is associated with viral variants containing an inactive pre-C region.",
RT Virology 176:596-603(1990).
RL -1 CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + [DNA] (N).
CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-phosphomonoester.
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CC EMBL: M32138; AAA45503.1; -.
DR PIR: C34773; JDUVAL.
DR InterPro; IPR001462; DNAPOL_viral_C.
DR InterPro; IPR000201; DNAPOL_viral_N.

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DR InterPro; IPR000477; RVTase.
DR Pfam; PF00336; DNA_pol_viral_C; 1.
DR Pfam; PF00242; DNA_pol_viral_N; 1.
DR Pfam; PF00078; tvc; 2.
DR ProDom; PD000814; DNAPOL_viral_C; 1.
DR Transferase; RNA-directed DNA polymerase; DNA-directed DNA polymerase;
KW Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SQ SEQUENCE 832 AA; 93589 MW; 236B4A3CCADD0829 CRC64;

Query Match 4.7%; Score 95; DB 1; Length 832;
Best Local Similarity 20.4%; Pred. No. 1.9; Indels 112; Gaps 19;
Matches 79; Conservative 47; Mismatches 150;

69 THDPFATOPQHYQNFLLYHCRHFPLLQDVPPSKC-----AQVFLLLVYKSSP-SNY 120
274 TYPSVSTFEKHSS-----GVAVELHNLPRNSARQSERPVSPCMWQFRNSKPCSDY 326
121 VRRL--LRRTWGRERKVRGLQLRL-----LFLVGTASNPHKAKVRLLEAQ 168
327 CLSHIVNLLEDWGPCAEHGHHRIRPTPARVTGVLVD--KNPNTESRLVDPFSQF 384
169 THGD-----ILQW---DFHDSFENLTLKQVFLQWQETRCANA 203
385 SRGNHRVSWKXAVPNQLSLTNLSSVLSLSDVSAAFVHLPLHPAAMPHLIVGSSGLS 444
204 SFV--LNGDDVFAHTDNMFYLODHDGRHLFVYQQLIQNVGIRAFWSK--YVVEVYVT 259
445 RYVARLSSDSRIFFHQGTQONLHD--SCSRNLVYSLTL-----YQTFGRKLHLVSHPIIL 499
260 QNEKYPYCCGGGFLSLRFTAA--ALRA-AHVLDIFPIDVFLG--MCLTELEGKPAK 313
500 GFRKIPMGVGLSPFLAQFTSALCSVYKRAFPICLASVYMDVVLGAKTVHHESLFTAV 559
314 HSGIRTSQVR-----APSQH-LSSFDPCEFRLDLLVIRFL 347
560 TNFLSLGSIHNLNPKTKRWGSLHFMGVYIGCYSLPQDHIIQIKICEF-----RKL 611
348 FYEKLMDALNQ-----PNLTG 366
612 PVNREIDMKVQCRIVGLGFAAPFTQCG 639

Search completed: June 14, 2004, 13:46:41
Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2004, 13:41:22 ; Search time 45 Seconds
(without alignments)
2608.284 Million cell updates/sec

Title: US-10-019-735-2

Perfect score: 2006
Sequence: 1 MKYLRRRNATLIALGAF.....LMMDALNPNTGNGOQIY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1998	99.6	372	4	Q9C0J2	Q9C0J2 homo sapien
2	1867	93.1	374	4	Q8WNR6	Q8WNR6 homo sapien
3	1321.5	65.9	372	11	Q8R0U2	Q8R0U2 mus musculu
4	1318.5	65.7	372	11	Q9D7Z2	Q9D7Z2 mus musculu
5	947	47.2	390	13	Q8UMM1	Q8UMM1 brachydantio
6	930	46.4	384	4	Q8TDX1	Q8TDX1 homo sapien
7	802	40.0	277	4	Q8TRZ4	Q8TRZ4 homo sapien
8	767	38.2	397	11	Q8K437	Q8K437 mus musculu
9	760	37.9	397	11	Q8K0J2	Q8K0J2 homo sapien
10	752	37.5	401	13	Q8NFI0	Q8NFI0 homo sapien
11	671.5	33.5	412	13	Q8UMM2	Q8UMM2 brachydantio
12	670	33.4	353	4	Q9G0H5	Q9G0H5 homo sapien
13	669	33.3	353	4	Q8WNR5	Q8WNR5 homo sapien
14	664	33.1	353	4	Q8WY02	Q8WY02 homo sapien
15	664	33.1	353	4	Q8N934	Q8N934 homo sapien
16	664	33.1	378	4	Q9C0J1	Q9C0J1 homo sapien

17	664	33.1	378	4	Q8N5W4	Q8N5W4 homo sapien
18	664	33.1	388	4	Q8ND21	Q8ND21 homo sapien
19	661	33.0	418	13	Q8UMM4	Q8UMM4 brachydantio
20	652	32.5	350	11	Q923H4	Q923H4 mus musculu
21	647	32.3	350	11	Q8UMM3	Q8UMM3 brachydantio
22	626	31.2	399	11	Q8V1I6	Q8V1I6 mus musculu
23	623.5	31.1	397	11	Q91V18	Q91V18 mus musculu
24	617.5	30.8	397	11	Q92222	Q92222 mus musculu
25	608	30.3	370	11	Q8BK98	Q8BK98 mus musculu
26	594	29.6	377	4	Q96EK0	Q96EK0 homo sapien
27	583	29.1	406	13	Q8UMM0	Q8UMM0 brachydantio
28	462.5	23.1	389	11	Q8K3I9	Q8K3I9 mus musculu
29	459.5	22.9	397	4	Q7Z7M8	Q7Z7M8 homo sapien
30	446.5	22.3	272	11	Q8BJ55	Q8BJ55 mus musculu
31	423.5	21.1	378	4	Q9BYG0	Q9BYG0 homo sapien
32	421.5	21.0	326	4	Q9Y5Z6	Q9Y5Z6 homo sapien
33	421.5	21.0	326	6	Q9WY77	Q9WY77 pongo pygma
34	421.5	21.0	326	11	Q54904	Q54904 mus musculu
35	421.5	21.0	376	11	Q8BGY6	Q8BGY6 mus musculu
36	417.5	20.8	376	11	Q810C6	Q810C6 mus musculu
37	416	20.7	305	11	Q91V52	Q91V52 mus musculu
38	416	20.7	305	11	Q920V5	Q920V5 mus spicille
39	414	20.6	289	6	Q865V2	Q865V2 macaca mula
40	414	20.6	377	6	Q864U8	Q864U8 sus scrofa
41	413.5	20.6	379	13	Q7F3S5	Q7F3S5 brachydantio
42	405.5	20.2	376	11	Q923K7	Q923K7 mus musculu
43	402.5	20.1	302	6	Q9N292	Q9N292 pongo pygma
44	363	18.1	409	11	Q91V19	Q91V19 mus musculu
45	363	18.1	422	4	Q9BZQ9	Q9BZQ9 homo sapien

ALIGNMENTS

RESULT 1	
Q9C0J2	PRELIMINARY; PRT; 372 AA.
AC Q9C0J2;	
DT 01-JUN-2001 (TrEMBLrel. 17, Created)	
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE Beta-1,3-N-acetylglucosaminyltransferase bGnt-3.	
GN BGN-3.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=2164825; PubMed=11042166;	
RA Shiraishi N., Natsume A., Togyachi A., Endo T., Akashima T.,	
RA Yamada Y., Imai N., Nakagawa S., Koizumi S., Sekine S., Narimatsu H.,	
RA Sasaki K.;	
RT "Identification and Characterization of Three Novel beta1,3-N-	
RT Acetylglucosaminyltransferases Structurally Related to the beta1,3-	
RT Galactosyltransferase Family."	
RL J. Biol. Chem. 276:3498-3507(2001).	
DR EMBL; AB049585; BAB21531.1; -	
DR GO; GO:0016020; C:membrane; IEA.	
DR GO; GO:0008378; F:galactosyltransferase activity; IEA.	
DR GO; GO:0004872; F:receptor activity; IEA.	
DR GO; GO:0016757; F:transferase activity; IEA.	
DR GO; GO:0005215; F:transporter activity; IEA.	
DR GO; GO:0004866; P:protein amino acid glycosylation; IEA.	
DR GO; GO:0006810; P:transport; IEA.	
DR InterPro; IPR002659; Glyco_trans_31.	
DR InterPro; IPR000531; TonB_box.	
DR Pfam; PF01762; Galactosyl_T_1.	
DR PROSITE; PS00430; TONB DEPENDENT_REC_1; 1.	
KW Glycosyltransferase; Transferase.	
SQ SEQUENCE 372 AA; 42534 MW; A6E3FE88B2FP00F10 CRC64;	
Query Match	99.6%; Score 1998; DB 4; Length 372;

[illegible]

RESULT 2

ID	Q8WMR6;	PRELIMINARY;	PRT;	374 AA.
AC	Q8WMR6;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Beta 1,6-GlcNAc-transferase.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bennett E.P.;			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AJ278961; CAC83374.1; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008378; F:galactosyltransferase activity; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR002659; Glyco_trans_31.			
DR	InterPro; IPR000531; TonB_boxC.			
DR	Pfam; PF01762; Galactosyl_T_1.			
DR	PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.			
DR	Transferrase.			
QO	SEQUENCE 374 AA; 42555 MW; ACCDF83C8520B151 CRC64;			

Query Match 93.1%; Score 1867; DB 4; Length 374;
 Best Local Similarity 94.9%; Pred. No. 8.1e-175;
 Matches 355; Conservative 1; Mismatches 16; Indels 2; Gaps 2

QY 1 MKYLRRRPNATLILGAFLLLSLSLSPCTCKVQEOBPAP1PEALAMPPTREAPAP 60
 Db 1 MKYLRRRPNATLILGAFLLLSLSLSPCTCKVQEOBPAP1PEALAMPPTREAPAP 60
 QY 61 CHANTSMYTHPEAFQPHVQNFLLYRHCRHPPLLDVPSPKCAQVFTLLVTKSSPSNY 120

D6	61	CHAMTSMWTHHDDFATQOPHOVNFLLYLRYCRHFFPLLODVPSPKCAOPVFLLILVIXSSPSNY	120
QY	121	VRRLRLRTWRERERVRGLRLRLFLVGTASPHKARKNRLLELEAOCHGDILOMDPHD	180
D6	121	VRRLRLRTWRERERVRGLRLRLFLVGTASPHKARKNRLLELEAOCHGDILOMDPHD	180
QY	181	SFNNLTLLKQVILFLOMOETRCA-NASF-VLNGDDVPAHTDNVFLYLODDPGRHLEFVGOL	238
D6	181	SFNNLTLLKQVILFVXARRQGA.PNALXRAOXGMMTSXAHTDNNVFLYLODDPGRHLEFVGOL	240
QY	239	IONNGPIRAPMSKYVPEVYTONEXYPPYCGGGFLISRFTAAALRRAAHVLDIFPIDVY	298
D6	241	IONNGPIRAPMSKYVPEVYTONEXYPPYCGGGFLISRFTAAALRRAAHVLDIFPIDVY	300
QY	299	FLGMCLELEGK.PASHSGIRTSGVAPSPQHLSSFPDPCFYRDLILLVHRFLPYEMLLMMDAL	358
D6	301	FLGMCLELEGK.PASHSGIRTSGVAPSPQHLSSFPDPCFYRDLILLVHRFLPYEMLLMMDAL	360
QY	359	NOPNLTGNOGTOIY 372	
D6	361	NOPNLTGNOGTOIY 374	

RESULT 3

LD	Q8R0U2	PRELIMITARY	PR1	3 / 2 AA.
AC	Q8R0U2			
DT	01-JUN-2002	(TREMBLrel. 21, Created)		
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	UDP-GlcNAc:betagal beta-1,3-N-acetylglucosaminyltransferase 3.			
GN	B3GNT3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC026418; AAH26418.1; -.			
DR	MGD; MGI:2152535; B3GNT3.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008378; F:galactosyltransferase activity; IEA.			
DR	GO; GO:0016757; F:galactase activity; transferring glycosyl. . .; IEA.			
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.			
DR	InterPro; IPR02659; Glyco_trans_31.			
DR	Pfam; PF01762; Galactosyl_T_1.			
DR	Transferrase; Glycosyltransferase.			
SW	SEQUENCE 372 AA; 42616 MW; 4887664C80AE75265 CRC64;			

Query Match	65.9%	Score 1321.5;	DB 11;	Length 372;
Best Local Similarity	67.0%;	Pred. No. 3.2e-121;		
Matches 248;	Conservative 39;	Mismatches 82;	Indels 1;	Gaps 1

QY	4	LRHRPNPTLLIAIAFAFTLLPSSL-VSPPTKQVQOPAIQBEALAMPPTPTAPAPCH	62
Db	3	LPQSPYEYELLIVALLVLLLLTSKSPSCSABRSKSPEDPNPCMGHGPRTTHPARCR	62
QY	63	ANTSMWTHDPFAPOBOHYQNFLLYRCHRPILLQDVPKCAQPVFLLVTKSPSNYVR	122
Db	63	ANLSYSSHPDFAGLEIHYADFLFYRHCROFPYLREBRVTKCAEPVLLLAIKSSPANYGR	122
QY	123	RELLARTGKREKXNGLOLRLLFLYGTJASNPHEARVYNLLLEAOTHGDILOMDFDSF	182
Db	123	KOMLTTPARERVRGAPLRRLFLVGSDDPQOARKYNLLEAKYGGILOMDFDSF	182
QY	183	FNULTIKOYLFLOMDETRCANASFVYVINGDDVPAHTDNMVFYLODHPGCHLFGOLLIONV	242
Db	183	FNULTIKOYLFLEMOLTYCTMASFVYVINGDDVPAHTDNMVTYLODHPDGHLPFGHLLIONV	242
QY	243	GPRAFWSKYVPEVATONERYPPYCGGGGFLISREFTAAALRRAAVLVDI FPIDDVFLGM	302

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DB 243 GPRVWSKYPFTLVMAEDRYPYCGGGFLLSRTVAALRAAAVLPMFPIDVFLGM 302
QY 303 CLEBGLKPAHSGIRTSVGRAPSOHLSSFPDCEFYRDLVHRFLPYEMLMDALNOPN 362
DB 303 CLQOQGLAPGTHSGVTAAGVFPSPRVSSPDCFYRDLVHRFLPYEMLMDALNOPQ 362
QY 363 LTCGNQTOY 372
DB 363 LTCGNQSPAY 372

RESULT 4
09D722 PRELIMINARY; PRT; 372 AA.
ID 09D722
AC 09D722
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 221000819PRik protein (Beta1,3 N-acetylglucosaminyltransferase-
DE 3)
GN 221000819PRik OR B3GNT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesl C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carrinzi P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
RA Guestincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Zhou D., Hennen T.;
RT "Mouse beta1,3 N-acetylglucosaminyltransferase-3.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK008674; BAB25624.1; -.
DR EMBL; AY037785; AAK6885.1; -.
DR MGI; MGI:2152535; B3gnt3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006378; F:galactosyltransferase activity; IEA.
DR GO; GO:0006486; F:protein amino acid glycosylation; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR InterPro; IPR002659; Glyco_trans_31.
DR Pfam; PF01762; Galactosyl_T; 1.
DR GlycoSylTransferase; Transferase.
SQ SEQUENCE 372 AA; 42572 MW; 5B38981D50A05C93 CRC64;

Query Match 65.7%; Score 1318.5; DB 11; Length 372;
Best Local Similarity 66.5%; Pred. No. 6,3e-121;
Matches 246; Conservative 41; Mismatches 82; Indels 1; Gaps 1;

QY 4 LRHRRNATLILALGAFLLFLSL-VSPPTCKVQSPALPAPALMPPTTPAPAPCH 62
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DB 3 LRPQSPYEILLVVALVLLILLTSKSPSCAPERSKPEBDNPGMAGHPRTHEARCR 62
QY 63 ANTSWTHDPATOPHOVONFLVYRCHRFPLLDVPPKCAQPVLLVITSSPENVYR 122
DB 63 ANLSVSHDFAFLPLHVDVDFYRCHCDFPVLRERVPKCAEPVLLAITSPPANYGR 122
QY 123 RELLRRTWGRKRVKRGLORLFLVGTASNPBEARKVNRLLLEAQTGGDILQMDPHDSF 182
DB 123 RQMLRTTWARKERVKCAPIRLFLVGSDDPQAKRCNNLLLEAOKGDILOMDHDSF 182
QY 183 FNLLTKQVLFLOQETRCANASFLVNGDDVFAHTDNWVFLQDHPGRHLFVGOLIQNV 242
DB 183 FNLLTKQVLFLEQQLYCTNAGSVLNGDDVFAHTDNWVFLQDHPDQHLFVGHLIQNV 242
QY 243 GPRVWSKYPFTLVMAEDRYPYCGGGFLLSRTVAALRAAAVLPMFPIDVFLGM 302
DB 243 GPRVWSKYPFTLVMAEDRYPYCGGGFLLSRTVAALRAAAVLPMFPIDVFLGM 302
QY 303 CLEBGLKPAHSGIRTSVGRAPSOHLSSFPDCEFYRDLVHRFLPYEMLMDALNOPN 362
DB 303 CLQOQGLAPGTHSGVTAAGVFPSPRVSSPDCFYRDLVHRFLPYEMLMDALNOPQ 362
QY 363 LTCGNQTOY 372
DB 363 LTCGNQSPAY 372

RESULT 5
08UWM1 PRELIMINARY; PRT; 390 AA.
ID 08UWM1
AC 08UWM1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-3-galactosyltransferase.
GN SSP4.
OS Brachydonia rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RX [1]
RP SEQUENCE FROM N.A.
RA Chou C.-M., Leu J.-H., Huang C.-J.;
RT "A family of novel genes encoding beta-3-galactosyltransferase from
RT zebrafish, zssp4 mRNA.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321830; AAL32298.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006378; F:galactosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006486; F:protein amino acid glycosylation; IEA.
DR InterPro; IPR002659; Glyco_trans_31.
DR Pfam; PF01762; Galactosyl_T; 1.
DR Transferase; Glycosyltransferase.
SQ SEQUENCE 390 AA; 45511 MW; E0DD359AAE71B07E CRC64;

Query Match 47.2%; Score 947; DB 13; Length 390;
Best Local Similarity 48.5%; Pred. No. 2.1e-84;
Matches 180; Conservative 66; Mismatches 103; Indels 22; Gaps 5;

QY 14 ILAIGAFLLLSL-----VSPPTCKVQSPALPAPALMPPTTPAPAPCH 62
DB 6 VVIALFLTGLMCLLTINKISKEDVSKCRIEEMNLNTPRTQTP--EPSSAPCV 63
QY 63 ANTSWTHDPATOPHOVONFLVYRCHRFPLLDVPPKCAQPVLLVITSSPENVYR 117
DB 63 ANTSWTHDPATOPHOVONFLVYRCHRFPLLDVPPKCAQPVLLVITSSPENVYR 122
QY 118 SNVRELLRRTWGRKRVKRGLORLFLVGTASNPBEARKVNRLLLEAQTGGDILQMD 177
DB 123 ENVDREVLRTWAEERLHKGVIRRVFLIGTSRSGFEKGRILRLIKLENNEKDILQMD 182
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Qy	178	FHSPFNRLTKOVLFLFLOMOTRCANNSFTVLNGDDVFAHNDNWFYLQ--DHDGRLRF	234
Db	183	FNDSPFNRLTKQILFLFLOMDMRRCPNARFLILDGDDIDFANFPNNIEYLQGEDNDGSRHLF	242
Qy	235	VGOLLQNVGGRIRAFWMSKYVYVEVVTQNERYPYPCGGGGGFLLSRFTAAALRRAAHVLDIFP	294
Db	243	TGHLGLKRVPIRKLRSKTYIPVQIHESNRIRPPICGGGGGFLLSGTATATTIKWSHSITLLP	302
Qy	295	IDDVFLGMCLELEGLKPSASHGIRTSGVAPRSCHLSSFDPCFYRDLILVHRFLPYEMILM	354
Db	303	IDDVVMGMCLEKAGLOPTEFHFGVRFTEGMNVPINKADRLDPCYREILVHRFQPHNIFVM	362
Qy	355	MDALNQPNLTLC	365
Db	363	WNEIQNPDLQC	373
RESULT 6			
Q8TDX1			
ID	08TDX1	PRELIMINARY;	PRT; 384 AA.
AC	08TDX1;		
DT	01-JUN-2002 (TREMBLrel, 21, Created)		
DT	01-JUN-2002 (TREMBLrel, 21, last annotation update)		
DT	01-JUN-2003 (TREMBLrel, 24, last annotation update)		
DE	Beta-1,3-N-acetylglucosaminyltransferase 6.		
GN	BETA3GNT6.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21935391; PubMed=11821425;		
RA	Iwai T., Inaba N., Naundorf A., Zhang Y., Gotoh M., Iwasaki H.,		
RA	Kudo T., Togeyachi A., Ishioka Y., Nakahishi H., Narimatsu H.;		
RT	"Molecular Cloning and Characterization of a Novel UDP-GlcNAc-6-		
RT	peptid beta1,3-N-Acetylglucosaminyltransferase (beta3Gn-T6), an Enzyme		
RT	Synthesizing the Core 3 Structure of O-Glycans.",		
RL	J. Biol. Chem. 277:12802-12809(2002).		
EMBL:	AB073740; BAB88882.1; --		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0008378; F:galactosyltransferase activity; IEA.		
DR	GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.		
DR	InterPro: IPR002659; P:protein amino acid glycosylation; IEA.		
DR	Pfam: PF01762; Galactosyl_T_1.		
DR	Transferrase; Glycosyltransferase.		
DR	SEQUENCE 384 AA; 42748 MW; 776C4577D3J008429 CRC64;		

	Query March	46.4%	Score 930;	DB 4;	Length 384;
	Best Local Similarity	52.8%;	Pred. No. 9.7e-83;		
	Matches 191;	Conservative 40;	Mismatches 119;	Indels 12;	Gaps 6
QY	15 LAIGAFLLLSLVSPPTC-----KNVEQPAIP-ELAMPTPTTRAPA-PCHTANTSM	67			
DB	17 LLVGVSFALQWFLQABRSPREERSPEEETPEGGTDPADADEPSELVPGPCVANNASA	76			
QY	68 VTHDPFATOPQOVHONFLLYRHCRRHPTLLQDVPSKCA--QPVLLLYTKSSPSNVVREL	125			
DB	77 NATADFEQLPARIQDFLYRHCRRHPTLLMDA-PAKCAAGRGVFLTLAVKSAPEHYERREL	135			
QY	126 LKRTWGERKKRYGLQLRLFLVLGTASNHEAR--KVNRLLELBAQTHGDIIQMFHDSFF	183			
DB	136 IIRRTWGERSGRSGPRVRLFLGTGPRDEARARIELVALERREHGDVLQMAFADFTL	195			
QY	184 NLTLKQVLFLOWOTRCANASFVLANGDDVDVAHTIDNNVFLYIQDHPGSHLFVGLIQNVG	243			
DB	196 NLTLKHLHLMDLNAARCPHARFLLISGDDVDVHANVAVRFLQAPGRHLPSGLMEGSV	255			
QY	244 PIRAFMSKYVPEVVTQNERPPYCGGGGLFSFTAALARRAHVLDIPIDIVFLGMC	303			
DB	256 PIDSMSKIVPPQIFGSAIVPYCSGGGLFSPTAALAAARHTPLFIDIVAGMC	315			

Qy	304	LELEGGKPAHSHSIRITSGVRAPQGHLSPPDPCYRDLIIVHRELIPYEMLLMPALNOPNL	363
Db	316	LEBAGLAPFGSHGSGIRPFPGVQLFEAQOOSFDPQMYRELIIVHRAPYEMLLMPALHSPAL	375
Qy	364	TC 365	
Db	376	SC 377	
RESULT 7			
Q8TAZ4			
ID	Q8TAZ4	PRELIMINARY;	PRT; 277 AA.
AC	Q8TAZ4;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Hypothetical protein (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas;		
RA	Straussberg R.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC025357; AAH25357.1; -.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0008378; F:galactosyltransferase activity; IEA.		
DR	GO; GO:0006486; P:protein amino acid glycosylation; IEA.		
DR	InterPro; IPR002659; GLYCO_trans_31.		
DR	Pfam; PF01762; Galactosyl_T; 1.		
KW	Hypothetical protein.		
FT	NON_TER		
SQ	SEQUENCE	277 AA; 30909 MW; E0CE4E50206CA531 CRC64;	

Query Match	40.0%	Score 802	DB 4	Length 277
Beet Local Similarity	57.4%	Pred. No. 2,4e-70.		
Matches 155	Conservative 33	Mismatches 78	Indels 4	Gaps 2
QY	100	PSKCA--QPVLLLVIKSPSNVYRRELRRTWGRERKVRGLQRLFLVNGTASNPHAR	157	
Db	1	PAKCAAGRGVLLLAIVKASAPHERRELRRTWGRERSYGRPVRRLLFLGTPEGDEAR	60	
QY	158	--KVNRLIEAQTGHDILLQWDFHDSFENLLTKOVLFLQWQETRCANASPYLNGDDVFA	215	
Db	61	AERLAELVALEAREHGVLLQWAFDTFLNTLLKHLHLLDMLAACPHARFLISGDVDFV	120	
QY	216	HTDMNVFLQDHDEGRHLFVGGLLQNGPIAFASKYVPEVYQNEKPYPCGGGGLL	275	
Db	121	HTANVVFELQAPGRHLFSGQLMEGSPVPLDSNKFVPPQLTPGSAIPYICGGGGLL	180	
QY	276	SRTFAALRRAAHVLDIFPIDVFLGNCLELEGKPKASHSGIRTSGVAPSPQHLSSPDP	335	
Db	181	SGPTARALRAAARHTPFPFIDDAVMGKCLBAGLAPSGHBSIRFPGVQLPBAQSSPDP	240	
QY	336	FYRDLVLRHFLPRFEMLLMDALNQWUTC	365	
Db	241	MYRELLVHRFAPYEMLLMWKALHSPALSC	270	
RESULT 8				
Q8K437	ID	PRELIMINARY;	PRT;	397 AA.
AC	Q8K437;			
DT	01-OCT-2002	(TREMBLrel. 22, Created)		
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Beta 1,3-N-acetylglucosaminyltransferase 7.			
GN	B3GN7.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ICR; TISSUE=Placenta;
 RC MEDLINE=22057328; PubMed=12061784;
 RA Kataoka K., Huh N.-H.;
 RT "A novel beta1,3-N-acetylglucosaminyltransferase involved in invasion
 of cancer cells as assayed in vitro."
 RL Biochem. Biophys. Res. Commun. 294:843-848(2002).
 DR EMBL: AF502429; AM61769.1; -.
 DR MGD; MGI:2384394; B3gnt7.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008378; F:galactosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro: IPR002659; Glyco_trans_31.
 DR Pfam: PF01762; Galactosyl_T; 1.
 DR Trnase; Trnase; 1.
 KW Trnase; Glycosyltransferase.
 SQ SEQUENCE 397 AA; 45366 MW; B7C45D0350DD87B CRC64;
 Query Match 38.2%; Score 767; DB 11; Length 397;
 Best Local Similarity 43.8%; Pred. No. 1e-66;
 Matches 154; Conservative 58; Mismatches 126; Indels 14; Gaps 5;
 QY 28 LVSPPTCKVQEQPPALPEALWPTPPRP-----APAPCHANTSMVTHPPAPQPOHVON 82
 DB 51 LVNPSFWMSSKQVAAPT-----PTVPRGPVMDVITTCNSINLTHQPFQSLPEPRQ 106
 QY 83 FLVYRCRHPFLIDVPPSKCAQPVFLLVTKSSPSYVRELLRRTGGERKVRGL--- 139
 DB 107 FLVYRCRYPEMLN-HPEKACADVLMVYVKSIVITQHDRREVIRQMGHEWSAGLGRG 165
 QY 140 QLRLLFLVGTASNPHEARKVRLLELAQTHGDILOWPHDSFNNLTQKVLFLQOETR 199
 DB 166 AVATLFLGTASQOERTHYQQLAYEDRLYADILQWDFLDSFNLTKHIFLKMLDIY 225
 QY 200 CANASFVNLGDDVFAHTDNMFYLODHPGRHLFVGQLIQNVGPTRAFWSKTYVEPVVT 259
 DB 226 CPVVPVFPKDDVDFVNPVTLFSLDRQOENLFGDVLKHAIRPKKDKNKYYIPAVMY 285
 QY 260 QNERYPYCGGGFLLSRFTAALRRAAVYLDIFPIDVFLGMCLEGLKPAHSGIRT 319
 DB 286 GKATYPPYAGGGFLLSGSLARQLHNACTLELFPIDVFLGMCLEGLGVKPGHSGFKT 345
 QY 320 SGVRAPOHLSDFPCFYRDLVLRFLPYEMLMMDALNQPLVTCGNGTOI 371
 DB 346 FGISRVRSSRMNKEPCFYRAMLVVHKLPAELLAMMDLVHS-NLTC5VKPQV 396
 RESULT 9
 Q8K0J2 PRELIMINARY; PRT; 397 AA.
 ID Q8K0J2
 AC Q8K0J2
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN B3GNT7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Colon;
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC031187; AAH31187.1; -.
 DR MGD; MGI:2384394; B3gnt7.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008378; F:galactosyltransferase activity; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.

DR InterPro: IPR002659; Glyco_trans_31.
 DR Pfam: PF01762; Galactosyl_T; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 397 AA; 45346 MW; F73932A35D4B182 CRC64;
 Query Match 37.9%; Score 760; DB 11; Length 397;
 Best Local Similarity 44.2%; Pred. No. 5.1e-66;
 Matches 153; Conservative 56; Mismatches 123; Indels 14; Gaps 5;
 QY 28 LVSPPTCKVQEQPPALPEALWPTPPRP-----APAPCHANTSMVTHPPAPQPOHVON 82
 DB 51 LVNPSFWMSSKQVAAPT-----PTVPRGPVMDVITTCNSINLTHQPFQSLPEPRQ 106
 QY 83 FLVYRCRHPFLIDVPPSKCAQPVFLLVTKSSPSYVRELLRRTGGERKVRGL--- 139
 DB 107 FLVYRCRYPEMLN-HPEKACADVLMVYVKSIVITQHDRREVIRQMGHEWSAGLGRG 165
 QY 140 QLRLLFLVGTASNPHEARKVRLLELAQTHGDILOWPHDSFNNLTQKVLFLQOETR 199
 DB 166 AVATLFLGTASQOERTHYQQLAYEDRLYADILQWDFLDSFNLTKHIFLKMLDIY 225
 QY 200 CANASFVNLGDDVFAHTDNMFYLODHPGRHLFVGQLIQNVGPTRAFWSKTYVEPVVT 259
 DB 226 CPVVPVFPKDDVDFVNPVTLFSLDRQOENLFGDVLKHAIRPKKDKNKYYIPAVMY 285
 QY 260 QNERYPYCGGGFLLSRFTAALRRAAVYLDIFPIDVFLGMCLEGLKPAHSGIRT 319
 DB 286 GKATYPPYAGGGFLLSGSLARQLHNACTLELFPIDVFLGMCLEGLGVKPGHSGFKT 345
 QY 320 SGVRAPOHLSDFPCFYRDLVLRFLPYEMLMMDALNQPLVTCG 365
 DB 346 FGISRVRSSRMNKEPCFYRAMLVVHKLPAELLAMMDLVHS-NLTC 390
 RESULT 10
 Q8NFLO PRELIMINARY; PRT; 401 AA.
 ID Q8NFLO
 AC Q8NFLO
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Beta 1,3-N-acetylglucosaminyltransferase 7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22057328; PubMed=12061784;
 RA Kataoka K., Huh N.-H.;
 RT "A novel beta1,3-N-acetylglucosaminyltransferase involved in invasion
 of cancer cells as assayed in vitro."
 RL Biochem. Biophys. Res. Commun. 294:843-848(2002).
 DR EMBL: AF502430; AM61770.1; -.
 DR Genew; HGNC:18811; B3GNT7.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008378; F:galactosyltransferase activity; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro: IPR002659; Glyco_trans_31.
 DR Pfam: PF01762; Galactosyl_T; 1.
 DR Trnase; Trnase; 1.
 KW Trnase; Glycosyltransferase.
 SQ SEQUENCE 401 AA; 45987 MW; CAF27F0A48DFE31 CRC64;
 Query Match 37.5%; Score 752; DB 4; Length 401;
 Best Local Similarity 40.8%; Pred. No. 3.2e-65;
 Matches 157; Conservative 64; Mismatches 136; Indels 26; Gaps 7;
 QY 13 LIALTAPFLUL-----FSLVSPPTCKVQEQPP-----ALPEALWPTPPRP 56
 DB 18 LTVAVTVFORSLLPQGFLOEPPPTLEPQAKQPNQOLVNPNNFWKPKDVAAPTPMAQO 77
 QY 57 AP-----APCHANTSMVTHPPAPQPOHVONFLVYRCRHPFLIDVPPSKCAQPVFL 109

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Db      78  GQAWDVTTTNCANINLTHQPMFQGLBPQFQFLYRHCRCYFPMILN-HPEKCGDYL 136
Qy      110  LVIITSSPBNVYRRELLRRTTNGRERKVRG---LQRLFLVGTASNPHARKVNLLEIE 166
Db      137  LVVVASVITQHDRREARIGTWRERQSAGGGAAYTTLGLGTASQOERTHYQOLLAWE 196
Qy      167  AQTGHDIIQWDPHDSFENLTLYKQVFLQOETRCANASFVLNGDDDVFAHTNMVFYLOD 226
Db      197  DRLYGDIILQMGFLDTFTFENLTKEIHFLKLDIYCHVVPFIKGGDDVFNPTNLLEFLAD 256
Qy      227  HDPSHLLFVGQLIQNVGFIRAFWSKYYVEVVTQNERYPYCGGGGFLLSRPTAALRRA 286
Db      257  RQPEMLFVGVDYLGHARPIRRKONKYYIGALYKASYPYAGGGGFLMAGSLARLHA 316
Qy      287  ANVLIFIPIDVFLGMCLEBGLKPAHSIGTSGVRASQHLSPDPCFYDILLVYRF 346
Db      317  CDTLELYPIDVFLGMCLEVLGVQPTAHBGFYFGISRNRSRMKKEPCFFRAMLVHKL 376
Qy      347  LPEYMLMDALNOPMLTCGNOTQI 371
Db      377  LPELLAMW-GLVHNSLTCRKLQV 400
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RESULT 11

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Q8UMW2  PRELIMINARY; PRT; 412 AA.
ID      O8UMW2
AC      O8UMW2;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Beta-3-galactosyltransferase.
GN      SSP3.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Chou C.-M., Leu J.-H., Huang C.-J.;
RT      "A family of novel genes encoding beta-3-galactosyltransferase from
RT      zebrafish, zssp3 mRNA."
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF312829; AAL32297.1; -.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0008378; F:galactosyltransferase activity; IEA.
DR      GO: GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR      GO: GO:0006486; P:protein amino acid glycosylation; IEA.
DR      InterPro: IPR002659; Glyco_trans_31.
DR      Pfam: PF01762; Galactosyl_T_1.
DR      Transferase: Glycosyltransferase.
KW      SEQUENCE 412 AA; 47812 MW; 80C554675A2CB00A CRC64;
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Best Local Similarity 40.8%; Pred. No. 2.7e-57;
Matches 127; Conservative 70; Mismatches 109; Indels 5; Gaps 3;

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Db      101  CTENSTITQIMFRLSPRFHFVLAHRHCYRYPMLN-HPEKCGGVVLVVVKSVEIEH 159
Qy      121  VRRELLRRTGGERKVGQLRLFLVGTASNPHARKVNLLEAQTGHDIIQWDPHD 180
Db      160  DRREAVRKTWKEGKIIGLKITLPLGTAPAKDSKMLQALVQVEDRTYGDIIQWDPHD 219
Qy      181  SFFNLTLLQVFLQOETRCANASFVLNGDDDVFAHTNMV---FYLDHDPGRHLFYQ 237
Db      220  TTFNLTLLKENVFLRFSIYCPDVPFIPKGGDDVFVHTNVLVELIGFRKEENKENVLIYGD 279
Qy      238  LIQNVGFIRAFWSKYYVEVVTQNERYPYCGGGGFLLSRPTAALRRAHVLDITPIDD 297
Db      280  AILEAKPIRNRQSKYFIPREL-YDKRYPPIYGGGGFLMSSQVARKVFTVSEVELYPIDD 338
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Qy      298  VFLGMCLEBGLKPAHSIGTSGVRASQHLSPDPCFYRDLILVHRELPEYMLMDA 357
Db      339  VFGMCLOKXNLIVPEVHLGFRFTFGIIRKVTRLNREBPCFFRDLIVHKLVPQDLKXMTL 398
Qy      358  LNOPMLTCGNQ 368
Db      399  VQNEBLSQARQ 409
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RESULT 12

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Q96QH5  PRELIMINARY; PRT; 353 AA.
ID      Q96QH5
AC      Q96QH5;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      Beta-1,3-galactosyltransferase.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Buthera; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Jensen M.A., Bennett E.P.;
RT      "Cloning of a new member of the beta 1,3 Galactosyltransferase family,
RT      b1.3gal-T7.",
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=20047730; PubMed=10580128;
RA      Amado M., Almeida R., Schwientek T., Clausen H.;
RT      "Identification and characterization of large galactosyltransferase
RT      gene families: galactosyltransferases for all functions1."
RL      Biochim. Biophys. Acta 1473:35-53(1999).
DR      EMBL; AJ130848; CAC45045.1; -.
DR      GO: GO:0016020; C:membrane; IEA.
DR      GO: GO:0008378; F:galactosyltransferase activity; IEA.
DR      GO: GO:0016757; F:transferase activity, transferring glycosyl. .; IEA.
DR      GO: GO:0006486; P:protein amino acid glycosylation; IEA.
DR      InterPro: IPR002659; Glyco_trans_31.
DR      Pfam: PF01762; Galactosyl_T_1.
DR      Glycosyltransferase: Transferase.
KW      SEQUENCE 353 AA; 39849 MW; B8F1128B75C78BBF CRC64;
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Query Match 33.4%; Score 670; DB 4; Length 353;
Best Local Similarity 42.9%; Pred. No. 3.1e-57;
Matches 148; Conservative 44; Mismatches 137; Indels 16; Gaps 6;

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Qy      22  LLRLSVSPPTCKVQEQPPIPEALAMPPTPRPAPRCHANMSWTHDPFAPOQHVQ 81
Db      16  LLGLGLFVRKTAKPAGDPTTHQPFMAPIPRHSRCF-PNHSVSA-----SLSPSRNR 69
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Db      116  LFLYRHCRAHNSIL-LPSSGCSKDTFLLAIKSQPGHVERRAAIRSGTWGVGMAGRQ 127
Qy      141  LRLFLVGTASNPHARKVNLLEAQTGHDIIQWDPHDSFENLTLYKQVFLQOETRC 200
Db      128  LKLVFLGLVNASADPA---QLAYESREPFDDIIQWQFTEDFFNLTKELHQLQMVVAAC 183
Qy      201  ANASFVLNGDDVFAHTDNMVFYLODHPGRLHFLVGQLIQNVGFIRAFWSKYYVEVVTQ 260
Db      184  PQAFMLKGGDDVVAHPVNVLEFIDGMDPADDLVGVYIRALDPNRUTKYKFIIPPSMYR 243
Qy      261  NERYPPYCGGGGFLLSRPTAALRRAHVLDITPIDVFLGMCLEBGLKPAHSIGRTS 320
Db      244  ATHRPYAGGGGYMSATYRRQLAIMEDALEPITDVPFGMCRRRLGLSPMHNAAGRTF 303
Qy      321  CVRAPSQHLSPDPCFYRDLILVHRELPEYMLMDALNOPMLTC 365
Db      304  GIRP---LDPLDCLYRGLILVHRLSLPLEMTWMALVTBGLKC 345
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DR pfam: PF01762; Galactosyl_T; 1.
KW Hypothetical protein.
SQ SEQUENCE 353 AA; 39819 MW; C6B4DE2092036192 CRC64;

Query Match 33.1%; Score 664; DB 4; Length 353;
Best Local Similarity 42.6%; Pred. No. 1.2e-56;
Matches 147; Conservative 43; Mismatches 139; Indels 16; Gaps 6;

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QY 82 NFLLYRHCHFPPLQDVPPSKCAQPVFLLLVIKSSPSNYRRELARTWGRERK-VRGIQ 140
DB 70 LFLTYRHCHNFSIL--LBPSSGCKDTFLLLAIKSQGHVERRAAIRSTWGRVGVARGGQ 127
QY 141 LRLPLVGTASNPHEARKVNRILLEAOTHDILQWDFHDSFENLTILKQVLFLOQOETRC 200
DB 128 LKLVFLGLVAGSAPPA----QLLAYESREPDILQWDFTEDEFNLTLKELHLQRWVVAAC 183
QY 201 ANASFLVNGDDVDVFAHTDNNVFYLODHPGRHLFVGQLIQNVGPTRAFWSKTYVPEVTQ 260
DB 184 PQAHFPLKGGDDVFAVFPVLEFLDGDMDPAODILVGDVIRQALPNRNTKVKYFIIPSMYR 243
QY 261 NERYPYCGGGGFLSRFTAALRRAAHVLDIPIDVFLGMCLBLEGLKPASHSGIRTS 320
DB 244 ATHYPPYAGGGGVMSRAIVRRLOAIMEDAELEPIDDVFGMCLRLGLSPMHAGFKTF 303
QY 321 GVRAPSOHLSSFPDCEYRDLILVHRFLPYEMLIMWDALNQPNLTG 365
DB 304 GIRRP---LDPRLPCLYRGILLVHRLSPLEMTMTMALVTDEGLKC 345

Search completed: June 14, 2004, 13:47:38
Job time : 46 secs

JOURNAL Patent: WO 0100848-A 2 04-JAN-2001;
KYOMA HAKKO KOGYO CO LTD, KATSUTOSHI SASAKI, NORIHIKO SHIRAIISHI,
AYUMI NATSUME, YOJI YAMADA, SATOSHI NAKAGAWA, SUSUMU SEKINE
COMMENT
OS Homo sapiens (human)
PN WO 0100848-A/2
PD 04-JAN-2001
PR 29-JUN-2000 WO 2000JP004304
PR 29-JUN-1999 JP 99P 183437 16-MAR-2000 JP 00P 074757 PI
KATSUTOSHI SASAKI, NORIHIKO SHIRAIISHI, AYUMI
NATSUME, YOJI YAMADA,
PI SATOSHI NAKAGAWA, SUSUMU SEKINE
PC C12N15/54, C12N9/10, C12N5/10, C12N1/21, A61K48/00, A61K45/00, PC
A61K39/395,
PC A61K35/00, A61K31/711, A61P35/00, A61P29/00, A01K67/027, A01H5/00,
PC G01N33/53,
PC G01N33/15, G01N33/05
CC
FH Key Location/Qualifiers.
1. .2205 Location/Qualifiers.
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 2205; DB 6; Length 2205;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCGAAGAACCGGACGAGCGCTGTTGATCTCCAGCCAGGGAGCTATTCCTAG 60
DB 1 GGCACAGAACCCGCAAGGCGCTGCTTGTTCACTCCAGCCAGGGAGCTATTCCTAG 60
QY 61 CAGCGGGCCAGACCCCAAGAGCGCCCAAGAGGCTCTAGAGGCCACCCCAAGCCTGCG 120
DB 61 CAGCGGGCCAGACCCCAAGAGCGCCCAAGAGGCTCTCTAGAGGCCACCCCAAGCCTGCG 120
QY 121 TGGCCAGATGAAGATCTCCGCGACCGGCGGCCCAATGCCACCTCATTTGGCCATG 180
DB 121 TGGCCAGATGAAGATCTCCGCGACCGGCGGCCCAATGCCACCTCATTTGGCCATG 180
QY 181 GGGCTTTCACTCTCTCTCTCTTCAAGTCTGTGTGTCACCACTTGCAGAGTTCAG 240
DB 181 GGGCTTTCACTCTCTCTCTCTTCAAGTCTGTGTGTCACCACTTGCAGAGTTCAG 240
QY 241 AGCAGCCACCGCGCATCCCGAGGCGCTGCGGCCCATCTCACCCACCGCGCGAGCC 300
DB 241 AGCAGCCACCGCGCATCCCGAGGCGCTGCGGCCCATCTCACCCACCGCGCGAGCC 300
QY 301 CGGCCCCGTGCATGCGAACACCTCTATGTACACCAACCGGACTTTCGCAAGCGCC 360
DB 301 CGGCCCCGTGCATGCGAACACCTCTATGTACACCAACCGGACTTTCGCAAGCGCC 360
QY 361 AGCAGTTCAAGATTTCTCTCTCTTCAAGTCTGTGTGTCACCACTTTCGCGAGAG 420
DB 361 AGCAGTTCAAGATTTCTCTCTCTTCAAGTCTGTGTGTCACCACTTTCGCGAGAG 420
QY 421 TGGCCCCCTCTAAGTGCAGCGGAGCTTCTCTGCTGTGTGATCAAGTCTTCCCTTA 480
DB 421 TGGCCCCCTCTAAGTGCAGCGGAGCTTCTCTGCTGTGTGATCAAGTCTTCCCTTA 480
QY 481 GCAACTATGTGTGCGCGCGAGCTGTGCGCGCGCATGTGGGCGCGAGCGCAAGATACGG 540
DB 481 GCAACTATGTGTGCGCGCGAGCTGTGCGCGCGCATGTGGGCGCGAGCGCAAGATACGG 540
QY 541 GTTTGACAGTGCCTCTCTCTCTCTGTTGGAGGACAGCTTCAACCCGACAGAGCGCCGA 600
DB 541 GTTTGACAGTGCCTCTCTCTCTCTGTTGGAGGACAGCTTCAACCCGACAGAGCGCCGA 600
QY 601 AGGTCAACCGGCTGTGAGCTGAGAGCAAGACTCAAGAGACATCTCTGACAGTGGACT 660
DB 601 AGGTCAACCGGCTGTGAGCTGAGAGCAAGACTCAAGAGACATCTCTGACAGTGGACT 660

QY 661 TCCACAGCTCTCTTTCAACCTCAAGCTCAAGCAGGTCTGTTCTTACAGTGGCAGAGA 720
DB 661 TCCACAGCTCTCTTTCAACCTCAAGCTCAAGCAGGTCTGTTCTTACAGTGGCAGAGA 720
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ACCESSION AX376220
VERSION AX376220.1 GI:19170501
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REFERENCE 1
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P., J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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 REFERENCE
 1 (bases 1 to 2210)

AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, O., Hass, P.E.,
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 Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
 Stinson, J., Vagstad, A., Vandlen, R., Watanabe, C., Weand, D., Woods, K.,
 Xia, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
 Goddard, A., Wood, W.I. and Godowski, P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 Genome Res. 13 (10), 2265-2270 (2003)
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 2 (bases 1 to 2210)
 Clark, H.F.
 TITLE Direct Submission
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 Sasaki, K., Shiraiishi, N., Natsume, A., Yamada, Y., Nakagawa, S. and
 Sekine, S.
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DB 112 CTCGCGGACACCGGCGCCCAATGCGACCTTATTTGCGCATGCGCGCTTTACCTCTCTC 171
QY 198 CTCCTTAGTCTGCTAGTGTACACCAACCACTTGCAAGGTCCAGGAGGACACCGGCGATC 257
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DB 292 AACACCTATAGGTGACACCAACCGGCGCTTGCGACGACCCCGAGACCGCGATGAGTAT 351
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DB 412 GCGGACCGCGCTCTTCTGCTGCTGCTGATCAAGTCTCCCTTAGACAACTATGTGCGCGC 471
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QY 1038 CTGAGACTTGAAGGAGCTGAAGCTGCTCCCAAGCGGCAATCCGACGCTTGGCGCG 1097
DB 1012 CTGAGACTTGAAGGAGCTGAAGCTGCTCCCAAGCGGCAATCCGACGCTTGGCGCG 1071
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QY 1877 AAGTTTGAAGACTCAGAGTTTCTGGGGTCTCATTTAGAGGCCCAATCCCTGTGTTCC 1936
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QY 1937 CAAGAAATTCAGAGAAACGACTGCGGGCTGGAATGATCTTTAATGGGCCCAAGCCAAAG 1996
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QY 1997 GCATATGCTCTCACTACTGCTGTGAGAAAGGAGATTCAGGTCTCTCAGAGCTCTCCCTC 2056
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Db	2032	ACCGATGATGTTTTCACAGATTACGGGGGAGACCGGGTGAGCCAGTGAACCCCTGTAAGCCC	20911
Qy	2117	CAGCTTCAGGCGCTCAGTGTCTGCCAGTCAAGCTTCACAGGCAATGTGTGATGGGACGCTT	2176
Db	2092	CAGCTTCAGGCGCTCAGTGTCTGCCAGTCAAGCTTCACAGGCAATGTGTGATGGGACGCTT	21511
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ACCESSION	AB049585		
VERSION	AB049585.1		
KEYWORDS	GI:12619295		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (sites)		
TITLE	Shiraiishi, N., Natsume, A., Togiyachi, A., Endo, T., Akahima, T., Yamada, Y., Imai, N., Nakagawa, S., Koizumi, S., Sekine, S., Narimatsu, H. and Sasaki, K.		
JOURNAL	Identification and characterization of three novel beta		
MEDLINE	1,3-N-acetylglucosaminyltransferases structurally related to the		
PUBMED	beta 1,3-galactosyltransferase family		
REFERENCE	J Biol Chem. 276 (5), 3498-3507 (2001)		
AUTHORS	2 (bases 1 to 2180)		
JOURNAL	Sasaki, K., Natsume, A. and Shiraiishi, N.		
MEDLINE	Direct Submission		
PUBMED	Submitted (02-OCT-2000) Katsutoshi Sasaki, The Tokyo Research		
REFERENCE	Laboratories, Kyowa Hakkō Kogyo Co., Ltd., Department of Molecular		
AUTHORS	Genetics; 3-6-6 Asahi-machi, Machida-shi, Tokyo 194-8533, Japan		
JOURNAL	(E-mail: kasaaki@kyowa.co.jp, Tel: 81-42-725-2555 (ex. 2150), Fax: 81-42-725-8330)		
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	RLLEAQTGHDIILOMDFHDSFNLITKQVLFLOMQRCAASFYLVGDDVDFAHTRD		
	NMVYVLODHDGRHLFVQGLIIONGPIPAFWSKYVPEVONRGPYPYGGGGFLSS		
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ORIGIN			
Query Match	95.7%	Score 2110.6;	DB 9; Length 2180;
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Matches 2124;	Conservative 0;	Mismatches 4;	Indels 1; Gaps 1;

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Db	112	CTCCGGGACCGGCGGCGCCCAATGCGACCCCTCATTTCTGGCATCGGCGCTTTGACCCCTCTC	171
QY	198	CTCTTCAAGTCTGCTAAGTGTACACACCCACTGACAGAGTTCAGAGACAGCACCGGCATC	257
Db	172	CTCTTCAAGTCTGCTAAGTGTACACACCCACTGACAGAGTTCAGAGACAGCACCGGCATC	231
QY	258	CCCGAGGCGCTGGGCGTGGCCGACCTCCACCCGACCCGGCCCGGCGCGGCGGCGCATGCC	317
Db	232	CCCGAGGCGCTGGGCGTGGCCGACCTCCACCCGACCCGGCGCGGCGGCGCGCATGCC	291
QY	318	AAACCTCTAATGATCACCCACCCGAGCTTTCGCACGACGCGCGACAGCATGTTAGAACTTC	377
Db	292	AAACCTCTAATGATCACCCACCCGAGCTTTCGCACGACGCGCGACAGCATGTTAGAACTTC	351
QY	378	CTCCTGTATCAGACACTGCGCGCACTTTCCTCCCTGCTGAGAGCGTGGCCCTCTAAGTGC	437
Db	352	CTCCTGTATCAGACACTGCGCGCACTTTCCTCCCTGCTGAGAGCGTGGCCCTCTAAGTGC	411
QY	438	GGCGAGCGGCTTCTTCGCTGCTGTGTATGAAGTCTCCCTAGCAATATGTTGGCGCG	497
Db	412	GGCGAGCGGCTTCTTCGCTGCTGTGTATGAAGTCTCCCTAGCAATATGTTGGCGCG	471
QY	498	GAGCTGCTGCGGCGCACGTTGGGGCGCGAGCGGCAAGGATCGGGGTTTTCAGCTGCGCTC	557
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QY	558	CTTCTCTGTGTGGGCGACAGCTTCCACCCGCGAGAGGCGCGCAAGTCAACCGGCTGCTG	617
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QY	738	AGCTTCGTGTCCAAACGAGGATGATGACGTCCTTGGCAACACAGACCAACATGTCCTTAC	797
Db	712	AGCTTCGTGTCCAAACGAGGATGATGACGTCCTTGGCAACACAGACCAACATGTCCTTAC	771
QY	798	CTGCAAGACCATGACCTTGGCGCGCACCTCTTCTGTTGGGGCACTGATCCAAAAGTGGGC	857
Db	772	CTGCAAGACCATGACCTTGGCGCGCACCTCTTCTGTTGGGGCACTGATCCAAAAGTGGGC	831
QY	858	CCCAATCCGGGCTTTTTGGAGCAAGTATATATGTGCAAGAGTGTGACTCAGAAATGAGGCG	917
Db	832	CCCAATCCGGGCTTTTTGGAGCAAGTATATATGTGCAAGAGTGTGACTCAGAAATGAGGCG	891
QY	918	TACCCACCCCTAATGTGGGGGTGTGTGAGCTTCTTGTCTGCCCTTCAACGCGCGCTGCCGTG	977
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QY	978	CGCGGTGTGCGCCATGTCTTGGACATCTTCCCAATGATATGTCTTCTTGGGTATGTCT	1037
Db	952	CGCGGTGTGCGCCATGTCTTGGACATCTTCCCAATGATATGTCTTCTTGGGTATGTCT	1011
QY	1038	CTGGAGCTTGGGAGCTGGAAGCTGCGCCCTCCACAGCGGCAATCCGCGACGTTGGCGTGGCG	1097
Db	1012	CTGGAGCTTGGGAGCTGGAAGCTGCGCCCTCCACAGCGGCAATCCGCGACGTTGGCGTGGCG	1071
QY	1098	GCTCCATTCGCAACCTGTCTCTCTTGTGACCCCTGCTCTTACCCGAGACTTGTCTGTGGT	1157
Db	1072	GCTCCATTCGCAACCGTGTCTCTCTTGTGACCCCTGCTCTTACCCGAGACTTGTCTGTGGT	1131
QY	1158	CACGCGTTCTAAGCTTATGAGATGCTGTCAATGTGGAGTGGCTGAAACAGCCCAACCTC	1217

Dp	1132	CACCGCTTCTACCTTATGAGTGTGCTCTCATGTGTGGATGGCTGTAACCAACGCCAACTCT	1191
Qy	1218	ACCTGGGCAATCAGACACAGATCTACTGAGTCAGACATCAGGGTCCCAAGCCTCTGGGCT	1277
Dp	1192	ACCTCGGGCAATCAGACACAGATCTACTGAGTCAGACATCAGGGTCCCAAGCCTCTGGGCT	1251
Qy	1278	CCTGTTTCCAGAGGAAGGGGGGCAACCTTCCCTCCAGGAAGCTGAGACCTTGTGGTCTG	1337
Dp	1252	CCTGTTTCCATATGGAAGGGGGGCAACCTTCCCTCCAGGAAGCTGAGACCTTGTGGTCTG	1311
Qy	1338	AGCATTAAGGAAGTGGCCAGGGAAGTTTGATGATGATGAATATCTGGCTGGCCGA	1397
Dp	1312	AGCATTAAGGAAGTGGCCAGGGAAGTTTGATGATGATGAATATCTGGCTGGCCGA	1371
Qy	1398	CTCCCTACACATCCCTTCAAAACCCACCTGTACTGTTCCAGCATCTTCCCTGGATGGCTGG	1457
Dp	1372	CTCCCTACACATCCCTTCAAAACCCACCTGTACTGTTCCAGCATCTTCCCTGGATGGCTGG	1431
Qy	1458	AGGAATCCAGAAATATATGATCTCTTTTGTGGCTGTATATGGCAGAAAGTGGCTGGG	1517
Dp	1432	AGGAATCCAGAAATATATGATCTCTTTTGTGGCTGTATATGGCAGAAAGTGGCTGGG	1491
Qy	1518	TAGAGTTCCAACTGTGATGCAATCCGTCCTGTTGAGTCAAAAGTCTTAATCTTCCCTGCTCT	1577
Dp	1492	TAGAGTTCCAACTGTGATGCAATCCGTCCTGTTGAGTCAAAAGTCTTAATCTTCCCTGCTCT	1551
Qy	1578	CACCTACTCAGAGAGGGAGTGTAAAGCATGATCACCCTGAGTGGTTTATGGCAGATTAAGC	1637
Dp	1552	CACCTACTCAGAGAGGGAGTGTAAAGCATGATCACCCTGAGTGGTTTATGGCAGATTAAGC	1611
Qy	1638	TCCGCTCTGACAGTCCAGGCCAGCCAGAAATCTGTGTCCATATAGAGCTGACCTGAGAA	1697
Dp	1612	TCCGCTCTGACAGTCCAGGCCAGCCAGAAATCTGTGTCCATATAGAGCTGACCTGAGAA	1671
Qy	1698	ATATCTTTCAGGCCCGAGAGAGAGGGGTCTGTATCTTAAACCTTTCTGGGTCTCAGACAA	1757
Dp	1672	ATATCTTTCAGGCCCGAGAGAGAGGGGTCTGTATCTTAAACCTTTCTGGGTCTCAGACAA	1731
Qy	1758	CTCAGAAAGTTGGGGGGATATCAGAGAGGTGTGGATTAAGGACCGCCCTCTTAATCTTG	1817
Dp	1732	CTCAGAAAGTTGGGGGGATATCAGAGAGGTGTGGATTAAGGACCGCCCTCTTAATCTTG	1791
Qy	1818	TGGGATCAAAATGCTGTAAATGTTGATGAGGTGTGGGAGAGAGGAGGCAAGTGT-CTTTGA	1876
Dp	1792	TGGGATCAAAATGCTGTAAATGTTGATGAGGTGTGGGAGAGAGGAGGCAAGTGTCTTTGA	1851
Qy	1877	AAGTTGTAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGACCCCAATCCTGTGTCTCC	1936
Dp	1852	AAGTTGTAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGACCCCAATCCTGTGTCTCC	1911
Qy	1937	CAAGAAATCAGAGAACAGACCTGGGGCTGAGATATCTTTAATGGGCCCAAGGCCAAG	1996
Dp	1912	CAAGAAATCAGAGAACAGACCTGGGGCTGAGATATCTTTAATGGGCCCAAGGCCAAG	1971
Qy	1997	GCATATGCTCTCACTATGCTGCTGGAGAGAGAGATTCAGGTCTCTCAGACGCTCCCTC	2056
Dp	1972	GCATATGCTCTCACTATGCTGCTGGAGAGAGAGATTCAGGTCTCTCAGACGCTCCCTC	2031
Qy	2057	ACCCAGTATGTTTTACAGATTAACGGGGGGGACCGGGTAGCCAGTACCCCTGTAGAGCCC	2116
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Qy	2117	CAGCTTCAGGCGCTCAGTGTCTGCCAGTCAAGCTTCAACAGCATTTGTATGGGGCAGGCTT	2176
Dp	2092	CAGCTTCAGGCGCTCAGTGTCTGCCAGTCAAGCTTCAACAGCATTTGTATGGGGCAGGCTT	2151
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DEFINITION	Human proteins having transmembrane domains and DNAs encoding these proteins.				
ACCESSION	BD063635	GI:22609238			
VERSION	BD063635.1	JP 2001508407-A/50.			
KEYWORDS	JP 2001508407-A/50.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Kato,S., Sekine,S., Kimura,T. and Kobayashi,M.				
TITLE	Human proteins having transmembrane domains and DNAs encoding these proteins				
JOURNAL	Patent: JP 2001508407-A 50 26-JUN-2001.				
COMMENT	SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC				
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QY	78	GGAAGCCCCCAGAGAGGCTCTCCAGAGCGAGCCCGAGACCTGGCTGGCCAGATGATGAT	137		
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QY	138	CTCCGGGACCGGGCGGCCCAATGCCACCTCATTTCTGGCCATGGGCGCTTTACCTCTCTC	197		
DB	127	CTCCGGGACCGGGCGGCCCAATGCCACCTCATTTCTGGCCATGGGCGCTTTACCTCTCTC	186		
QY	198	CTCTTCAAGTCGTAGTGTACCAACCCAGCTGAGAGGTCGACGAGAGGACGACCGGGAGTC	257		
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QY	258	CCCGAGGCGCTTGGCTGGCCACTTCAACCCAGCCGCGCAGACCCCGGCGCCCGTCCATGGC	317		
DB	247	CCCGAGGCGCTTGGCTGGCCACTTCAACCCAGCCGCGCAGACCCCGGCGCCCGTCCATGGC	306		
QY	318	AAGACCTTATGTGACACCAACCGGAGCTTGGCCAGCAGACGCGGAGAGGTCGTAAGATTC	377		
DB	307	AAGACCTTATGTGACACCAACCGGAGCTTGGCCAGCAGACGCGGAGAGGTCGTAAGATTC	366		
QY	378	CTCTCTATACAGACTGCGCGCACTTTCCTCTGCTGACGAGACGTCGCCCTCTAAGTGC	437		
DB	367	CTCTCTATACAGACTGCGCGCACTTTCCTCTGCTGACGAGACGTCGCCCTCTAAGTGC	426		
QY	438	GCGGACCGCGTCTTCTGCTGCTGTGTGATTAAGTCTCTCCCTTAGCAATATGTGGCCCG	497		
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QY	498	GAGCTGTGCGGCGACGTGGGGCGGAGCGGAGCGAAGTACGGGGTTTGGAGCTGCGCTTC	557		
DB	487	GAGCTGTGCGGCGACGTGGGGCGGAGCGGAGCGAAGTACGGGGTTTGGAGCTGCGCTTC	546		
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Qy 1338 AGCATTAAGGAGGAGCCAGGAGAGGTTGAGTGTGATGATGATGATGATGATGATGATGATGAT 1397
Db 1327 AGCATTAAGGAGGAGCCAGGAGAGGTTGAGTGTGATGATGATGATGATGATGATGATGATGAT 1386
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Db 1387 CTCCTACACATCTTCAAAACCACTGTGACTGTTCCAGACATCTTCCCTGATGTGCTG 1446
Qy 1458 AGGAATCTCAGAAATATGATCTTCTTGTGTGCTGCTTAATGAGAGAGTCCCTGTG 1517
Db 1447 AGGAATCTCAGAAATATGATCTTCTTGTGTGCTGCTTAATGAGAGAGTCCCTGTG 1506
Qy 1518 TTAGAGTTTCAACTGTGTGATGATCTTCCGCTTGTGATGATGATGATGATGATGATGATGAT 1577
Db 1507 TTAGAGTTTCAACTGTGTGATGATCTTCCGCTTGTGATGATGATGATGATGATGATGATGAT 1566
Qy 1578 CACCTACTACAGACGGAGTGTAAAGACAGTCACTGACAGTGTGTTAATGAGAGATAGC 1637
Db 1567 CACCTACTACAGACGGAGTGTAAAGACAGTCACTGACAGTGTGTTAATGAGAGATAGC 1626
Qy 1638 TCCGTCGTAGGTTCCAGGCGCAGGCAAGAACTCCTGTGTTCACATAGAGCTGACGTAGAA 1697
Db 1627 TCCGTCGTAGGTTCCAGGCGCAGGCAAGAACTCCTGTGTTCACATAGAGCTGACGTAGAA 1686

Qy 1698 ATATCTTTAGCCACAGAGAGAGGGGTCCTGATCTTAACCTTCTCTGGGCTCAGACAA 1757
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Qy 1758 CTCAGAAAGTTGGGGGATACACAGAGGTGTGAAATAGAACCGCCCTCTTAATTG 1817
Db 1747 CTCAGAAAGTTGGGGGATACACAGAGGTGTGAAATAGAACCGCCCTCTTAATTG 1806
Qy 1818 TGGGATCAAAATGCTGTAATGTGTGAGAGTGTGGGCAAGAGAGGAGGCAAGTGT-CTTTGA 1876
Db 1807 TGGGATCAAAATGCTGTAATGTGTGAGAGTGTGGGCAAGAGAGGAGGCAAGTGTCTTTGA 1866
Qy 1877 AAGTTGAGAGCTCAGAGCTTCTGGGCTCTGATGAGAGCCCATCCCTGTGTTCC 1936
Db 1867 AAGTTGAGAGCTCAGAGCTTCTGGGCTCTGATGAGAGCCCATCCCTGTGTTCC 1926
Qy 1937 CAAGAAATTCAGAGACAGACCTGGGCTGAAATGATCTTTAATGAGCCCAAGCAACAG 1996
Db 1927 CAAGAAATTCAGAGACAGACCTGGGCTGAAATGATCTTTAATGAGCCCAAGCAACAG 1986
Qy 1997 GCATATGCTCACTACTGCTGAGAGAGGAGATTCAGGTCTCTCAGACGCTCCCTC 2056
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Db 2047 ACCCAGTATGTTTAAAGATTAACGGGGGAGACGGGGAGACAGTGAACCCCTGACAGCCC 2106
Qy 2117 CAGCTTCAGAGCCTCAGTGTCTGCAAGTCAAGCTTCAAGGCAATGATGATGAGGACAGCTT 2176
Db 2107 CAGCTTCAGAGCCTCAGTGTCTGCAAGTCAAGCTTCAAGGCAATGATGATGAGGACAGCTT 2166
Qy 2177 GGGGAATTAATAATTTTGTG 2196
Db 2167 GGGGAATTAATAATTTTGTG 2186

RESULT 7
BD141469
LOCUS BD141469 2186 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of constructing antibody by gene immunity.
ACCESSION BD141469
VERSION BD141469.1 GI:23236414
KEYWORDS WO 0208416-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2186)
AUTHORS Kato,S., Nagata,N., Fujimura,N., Kobayashi,M., Ito,K. and
Ishizuka,Y.
TITLE Method of constructing antibody by gene immunity
JOURNAL Patent: WO 0208416-A 8 31-JAN-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP. SEISHI KATO,NAOKI NAGATA, NAOKO
FUJIMURA, MIDORI KOBAYASHI,KOICHI ITO,YOSHIKO ISHIZUKA
COMMENT OS Homo sapiens (human)
PN WO 0208416-A/8
PD 31-JAN-2002
PF 24-JUL-2001 WO 2001JP006371
PR 24-JUL-2000 JP 00P 222743.24-AUG-2000 JP 00P 254407 PI
SEISHI KATO,NAOKI NAGATA,NAOKO FUJIMURA,MIDORI KOBAYASHI, PI
KOICHI ITO,
PI YOSHIKO ISHIZUKA
PC C12N15/09,C07K16/00
CC Method of constructing antibody by gene immunity FH key
Location/Qualifiers (118)..(1236).
FT CDS
FEATURES
source Location/Qualifiers
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QY	1458	AGGAATCCAGAAATATGATCTTCTTTTGGCTGTATATGGCAGAAAGTGGCTGG	1517
Db	1447	AGGAATCCAGAAATATGATCTTCTTTTGGCTGTATATGGCAGAAAGTGGCTGG	1506
QY	1518	TAGAGTTCCAACTGTGATGATCCGTCCTGTTTGAATCAAACTTTACTTCCCTGCTCT	1577
Db	1507	TAGAGTTCCAACTGTGATGATCCGTCCTGTTTGAATCAAACTTTACTTCCCTGCTCT	1566
QY	1578	CACCTTACTACAGAGGGATGCTTAAGACATGACCTGCGATGGTTTAAATGGCAGTAAGC	1637
Db	1567	CACCTTACTACAGAGGGATGCTTAAGACATGACCTGCGATGGTTTAAATGGCAGTAAGC	1626
QY	1638	TCCGTCGTGATCCAGGCGCAGAAACTCCTGTGTCCATAGAGCTGACGTGAGAA	1697
Db	1627	TCCGTCGTGATCCAGGCGCAGAAACTCCTGTGTCCATAGAGCTGACGTGAGAA	1686
QY	1698	ATATCTTTTCCAGCCAGAGAGAGGGGTCTGTATCTTTAACCTTTCTGCGTCTCAGACAA	1757
Db	1687	ATATCTTTTCCAGCCAGAGAGAGGGGTCTGTATCTTTAACCTTTCTGCGTCTCAGACAA	1746
QY	1758	CTCAGAAAGTTGGGGGATACCAAGAGATGATGAAATAGAACCGCCCTCTTACTTG	1817
Db	1747	CTCAGAAAGTTGGGGGATACCAAGAGATGATGAAATAGAACCGCCCTCTTACTTG	1806
QY	1818	TGGGATCAATGCTGTATGTGTGAGAGTGTGGCAGAGAGAGGAGCAAGTGT-CTTTGA	1876
Db	1807	TGGGATCAATGCTGTATGTGTGAGAGTGTGGCAGAGAGAGGAGCAAGTGT-CTTTGA	1866
QY	1877	AAGTTGTGAGAGTCTGAGATTTCTGGGTCCTCATTTAGAGCCCTTCTGTGTCTCC	1936
Db	1867	AAGTTGTGAGAGTCTGAGATTTCTGGGTCCTCATTTAGAGCCCTTCTGTGTCTCC	1926
QY	1937	CAGAAATTCAGAGAACAGACATGGGGCTGGAATGATCTTTAATGGGCCCAAGGCCAAG	1996
Db	1927	CAGAAATTCAGAGAACAGACATGGGGCTGGAATGATCTTTAATGGGCCCAAGGCCAAG	1986
QY	1997	GCATATGCTCTACTATCTGCTCGAGAGAGGAGATTCAGATCTCTCAGACGCTCCCTC	2056
Db	1987	GCATATGCTCTACTATCTGCTCGAGAGAGGAGATTCAGATCTCTCAGACGCTCCCTC	2046
QY	2057	ACCCAGTATGTTTAAAGATTAACGAGGAGACCGGGGTGAGCCAGTGAACCCCTGCAAGCCC	2116
Db	2047	ACCCAGTATGTTTAAAGATTAACGAGGAGACCGGGGTGAGCCAGTGAACCCCTGCAAGCCC	2106
QY	2117	CAGCTTCAGGCTCAGATGTGTCAGATCAAGCTTCAAGGCAATTGATGGGGCAGCCTT	2176
Db	2107	CAGCTTCAGGCTCAGATGTGTCAGATCAAGCTTCAAGGCAATTGATGGGGCAGCCTT	2166
QY	2177	GGGGAATATTAATTTTGTG 2196	
Db	2167	GGGGAATATTAATTTTGTG 2186	

RESULT 9
 AX136253 2198 bp DNA linear PAT 30-MAY-2001
 LOCUS AX136253
 DEFINITION Sequence 175 from Patent EP1067182.
 ACCESSION AX136253
 VERSION AX136253.1 GI:14272659
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKAYOVA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
 AUTHORS Hayashi, K.
 TITLE Secretory protein or membrane protein

JOURNAL	Patent: EP 1067182-A 175 10-JAN-2001;	
HELI	Helix Research Institute (JP)	
FEATURES	Location/Qualifiers	
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ORIGIN		
Query Match	94.6%; Score 2087; DB 6; Length 2198;	
Best Local Similarity	99.4%; Pred. No. 0; Mismatches 10; Indels 3; Gaps 2;	
Matches 2116; Conservative		
QY	78 GGAGCGCGCCAGAGAGCTCTCAGGCGAGACCCAGACCTGAGCTGGCCAGATGAAGTAT	137
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QY	138 CTCGGCAACCGCGCGCCCAATGCAACCTCATTTGAGCATGAGGCTTTTCAACCTCTCTC	197
Db	132 CTCGGCAACCGCGCGCCCAATGCAACCTCATTTGAGCATGAGGCTTTTCAACCTCTCTC	191
QY	198 CTCTTCACTGTCTGTATGTGTCAACACCTGCAAGTGTCAAGAGACGACCGGCGATC	257
Db	192 CTCTTCACTGTCTGTATGTGTCAACACCTGCAAGTGTCAAGAGACGACCGGCGATC	251
QY	258 CCGAGGCGCTGGCGCCATCTCAGCCACCGCCAGACCCGCGCCGCGCATGCC	317
Db	252 CCGAGGCGCTGGCGCCATCTCAGCCACCGCCAGACCCGCGCCGCGCATGCC	311
QY	318 AACACCTTATGATGATCAACCAACCGGACCTTGGCAGCAGCGCAGACGTTCAAGATTC	377
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QY	378 CTCTGTATACAGACATGCGCGCATCTTCCCTGCTGCAAGAGTGTGCTTAAATGTC	437
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QY	678 AACCTCAGCTCAAGAGAGTCTTCTTTTACAGTGGCAGAGACAAAGTGGCCAAAGCC	737
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QY	738 AGCTTGTGTCTCAACGGGAGATGATGAGTCTTTCACACAGACAAATGCTTCTTAC	797
Db	732 AGCTTGTGTCTCAACGGGAGATGATGAGTCTTTCACACAGACAAATGCTTCTTAC	791

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 DB 852 CCCATCCGGGCTTTTGGAGCAAGTACTATGTGCGAGAGGTGTGATCTCAAGATGAGCG 911
 QY 918 TACCCACCTTATTTGGGGGTGTGTGCTTGTGCTCCGCTTCAAGGCGGCTGGCCCTG 977
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 DB 1152 CACCGCTTCTTACCTTATGATGCTGCTGATGAGGAGTGGGCTGAACCAAGCCCAACTC 1211
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 DB 1212 ACCTGCGGCAATGAGACAGATCTACTGATGATGATGATGATGATGATGATGATG 1271
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 DB 1632 TCCGTCTGAGTTTCAAGGCGAGCAAACTCTGTGTCAATAGAGCTGACGTGAGAA 1689
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QY 1877 AAGTTGAGAGCTCAGAGTTTCTGGGGTCTCTATTAGAGAGCCCATCTGTGTCTCC 1936
 DB 1870 AAGTTGAGAGCTCAGAGTTTCTGGGGTCTCTATTAGAGAGCCCATCTGTGTCTCC 1929
 QY 1937 CAAGATTCAG 1996
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 QY 2117 CAGCTTCAGGCTCAGTGTCTGCGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2176
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 BD123579 2198 bp DNA linear PAT 18-SEP-2002
 LOCUS
 DEFINITION
 Secretory protein or membrane protein.
 ACCESSION
 BD123579
 VERSION
 BD123579.1 GI:23218524
 KEYWORDS
 JP 2002017376-A/88
 SOURCE
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 2198)
 AUTHORS
 Oca,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.
 TITLE
 Secretory protein or membrane protein
 JOURNAL
 Patent: JP 2002017376-A 88 22-JAN-2002;
 HELIX RESEARCH INSTITUTE
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002017376-A/88
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253173
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
 PI SUGIYAMA,
 PI KOJI HAYASHI
 PC
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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 PC C12P21/02, C12Q1/68//C12P21/08, C12N15/00, C12N5/00 CC
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 Query Match 94.6%; Score 2087; DB 6; Length 2198;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 2116; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
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 DB 72 GGAGCGGCGGAG 131
 QY 138 CTCGGGACCGGCGGCGGAG 197

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Db	192	CTCTTCAGTCGTGTATGTGTCAACCAACCACTCGCAAGGTCCAGAGGACGCAACCGGAGATC	251
QY	258	CCCGAGGCCCTGGCCCTGGGCCCACTCCACCCCGCCAGCCCGGCCCCGTCGTCATGCC	317
Db	252	CCCGAGGCCCTGGCCCTGGGCCCACTCCACCCCGCCAGCCCGGCCCCGTCGTCATGCC	311
QY	318	AAACCTCTAATGATCAACCAACCGAGACTTTCGACGACGACCGGAGACGTTCAAGATTC	377
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QY	498	GAGCTGCTGCGCGCGACGTGG33CCGCGAGCGCAAGTAACGG3GTTTTCAGCTGCGCTTC	557
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Db	552	CTCTTCTGTGTGGGACAGCCTTCAACCGCGCAAGAGGCCCGAAGGTCAACCGGCTGCTG	611
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QY	678	AACCTCAAGCTCAAGCAGGTCTCTGTCTTAAGTGGCAAGGACAAAGTGCAGCAACGCGC	737
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QY	738	AGCTTCGTGCTCAACGGGAGTATGACGTCCTTTCGACACAGACAAACATGTCTTCTAC	797
Db	732	AGCTTCGTGCTCAACGGGAGTATGACGTCCTTTCGACACAGACAAACATGTCTTCTAC	791
QY	798	CTGCGAGACATGACACCTTGCGGCCCACTCTTCTGTGTGGGCAACTGATCCAAACGTGGGC	857
Db	792	CTGCGAGACATGACACCTTGCGGCCCACTCTTCTGTGTGGGCAACTGATCCAAACGTGGGC	851
QY	858	CCCATCCCGGGCTTTTTCGAGCAAGTACTATGTGCCAGAGAGTGTGTCTCAGAAATGAGCGG	917
Db	852	CCCATCCCGGGCTTTTTCGAGCAAGTACTATGTGCCAGAGAGTGTGTCTCAGAAATGAGCGG	911
QY	918	TACCACTCTATTTGTGTGG3GTGTGGCTTTCGTGTCGCCGCTTCAACGGCCGCTGCCCTG	977
Db	912	TACCACTCTATTTGTGTGG3GTGTGGCTTTCGTGTCGCCGCTTCAACGGCCGCTGCCCTG	971
QY	978	CGCGGTGTCGCCCATGTCTGTGGACATCTTCCCATTAAGTATGTCCTTCGTGGTATGTGT	1037
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QY	1038	CTGAGCTTGAAGGACTGAAGCTGACCTCCACAGCGGCATTCGACGCTTGG3CTGGCGG	1097
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QY	1098	GCTCCATGTGCAACACGTGCTCTCTTTTGAACCCCTGCTCTTACCGAGACTGTGCTGGTG	1157
Db	1092	GCTCCATGTGCAACACGTGCTCTCTTTTGAACCCCTGCTCTTACCGAGACTGTGCTGGTG	1151
QY	1158	CACCGCTTCTACCTTATGAGATGTGCTCAATGTGGATGCGCTAAACAAGCCCAACCTC	1217
Db	1152	CACCGCTTCTTACCTTATGAGATGTGCTCAATGTGGATGCGCTAAACAAGCCCAACCTC	1211
QY	1218	ACCTGCGGCATTCAGACACAGATCTACTGAAGTCAAGATCAAG3GTCCTCAAGCCTCTGG3CT	1277
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LOCUS	DEFINITION	2198 bp	mRNA	linear	PRI 03-SEP-2002
ACCESSION	AK075466	AK075466	AK075466	AK075466	AK075466
VERSION	AK075466.1	GI:22761569			
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QY	1458	AGGAACCTCAGAAAAATATGCAATCTCTTTTGTGGCTGCTATGAGCAAAATGCTGTGC			1517b
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QY	1518	TAGAGTTCCAACTGTGATGCATCCGTCCGTTTGATGATCAAAATCTTACTTCCCTGCT			1577b
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QY	1578	CACCTACTCAGAGAGGGAGTCTTAAGCAGTGCACCTGAGAGTGTTATATGACATATAGC			1637b
Db	1572	CACCTACTCAGAGAGGGAGTCTTAAGCAGTGCACCTGAGAGTGTTATATGACATATAGC			1631b
QY	1638	TCCGTTCTCAGTTCCAGGCGCAGCCAGAAACTCTGTGTCCACATAGAGCTGACGTGAA			1697b
Db	1632	TCCGTTCTCAGTTCCAGGCGCAGCCAGAAACTCTGTGTCCACATAGAGCTGACGTGAA			1689b
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ACCESSION	AK075466
VERSION	AK075466.1 GI:22761569

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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

oligo capping; file (full insert sequence).
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Oca, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,
Ishii, S., Saito, K., Yamamoto, J., Makamatsu, A., Nagai, T.,
Makamura, Y., Nagahari, K., Sugano, S. and Ieogai, T.
HRI human cDNA sequencing project
Unpublished
2 (bases 1 to 2198)
Ieogai, T. and Yamamoto, J.
Direct Submission
Submitted (20-MAR-2002) Takao Ieogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
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DEFINITION Sequence 131 from Patent EP1067182.
ACCESSION AX136209
VERSION AX136209.1 GI:14272617
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
Ota,T., Iwoga,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
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Helix Research Institute (JP)
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Best Local Similarity 99.5%; Pred. No. 8.7e-266;
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ACCESSION BD123557
VERSION BD123557.1 GI:23218502
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1 (bases 1 to 1999)
Oca,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
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ORIGIN

Query Match 62.1%; Score 1368.4; DB 6; Length 1999;
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Matches 1363; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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(without alignments)
10955.879 Million cell updates/sec

Title: US-10-019-735-6
Perfect score: 2205
Sequence: 1 ggcacgagacccgcaagcg.....aaatttgtgaacttgg 2205

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jun04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2205	100.0	2205	4	AAF29256	Aaf29256 Human bet
2	2124.8	96.4	2427	5	ABV22526	Abv22526 Human pro
3	2124.8	96.4	2427	5	ABV28341	Abv28341 Human pro
4	2119.8	96.1	2210	4	AAS46068	Aas46068 Human DNA
5	2119.8	96.1	2210	7	ABX78671	Abx78671 Human PRO
6	2119.8	96.1	2210	7	ACA75643	Aca75643 Novel hum
7	2119.8	96.1	2210	7	ACA71123	Aca71123 Human sec
8	2119.8	96.1	2210	7	ACC87651	Acc87651 Human sec
9	2119.8	96.1	2210	7	ACCD87037	Accd87037 Human sec
10	2119.8	96.1	2210	7	ACCD4210	Accd4210 Human sec
11	2119.8	96.1	2210	7	ACA69541	Aca69541 cDNA enco
12	2119.8	96.1	2210	7	ACA90386	Aca90386 Novel hum
13	2119.8	96.1	2210	7	ACC89493	Acc89493 Human sec
14	2119.8	96.1	2210	7	ACA98284	Aca98284 Novel hum
15	2119.8	96.1	2210	7	ACA93926	Aca93926 Human sec
16	2119.8	96.1	2210	7	ACD15319	Accd15319 Human sec
17	2119.8	96.1	2210	7	ACCD8906	Accd8906 Human sec
18	2119.8	96.1	2210	7	ACC96826	Acc96826 Human sec
19	2119.8	96.1	2210	7	ACF15547	Accf15547 Human sec
20	2119.8	96.1	2210	7	ACA72914	Aca72914 Human PRO
21	2119.8	96.1	2210	7	ACD03086	Accd03086 Novel hum
22	2119.8	96.1	2210	7	ACD01901	Accd01901 Novel hum
23	2119.8	96.1	2210	7	ACA92093	Aca92093 Novel hum

24	2119.8	96.1	2210	7	ACA89518	Aca89518 cDNA enco
25	2119.8	96.1	2210	7	ACA73528	Aca73528 Human sec
26	2119.8	96.1	2210	7	ACA05843	Aca05843 Human sec
27	2119.8	96.1	2210	7	ACA66677	Aca66677 cDNA enco
28	2119.8	96.1	2210	7	ACF20252	Accf20252 Human sec
29	2119.8	96.1	2210	7	ACF19638	Accf19638 Human sec
30	2119.8	96.1	2210	7	ACD21926	Accd21926 Human sec
31	2119.8	96.1	2210	7	ACF13091	Accf13091 Human sec
32	2119.8	96.1	2210	7	ACD25194	Accd25194 Human sec
33	2119.8	96.1	2210	7	ACF00243	Accf00243 Human sec
34	2119.8	96.1	2210	7	ACA72300	Aca72300 Novel hum
35	2119.8	96.1	2210	7	ACD04824	Accd04824 Novel hum
36	2119.8	96.1	2210	7	ACD18285	Accd18285 Human sec
37	2119.8	96.1	2210	7	ACD08292	Accd08292 Human sec
38	2119.8	96.1	2210	7	ACA88726	Aca88726 Novel hum
39	2119.8	96.1	2210	7	ACA70168	Aca70168 Human sec
40	2119.8	96.1	2210	7	ACD12390	Accd12390 Novel hum
41	2119.8	96.1	2210	7	ACD74305	Accd74305 Human sec
42	2119.8	96.1	2210	7	ACD15933	Accd15933 Human sec
43	2119.8	96.1	2210	7	ACD25501	Accd25501 Novel hum
44	2119.8	96.1	2210	7	ACD17978	Accd17978 Human sec
45	2119.8	96.1	2210	7	ACC88265	Acc88265 Human sec

ALIGNMENTS

RESULT 1
AAF29256 standard; cDNA; 2205 BP.
XX

AC AAF29256;
XX

DT 17-APR-2001 (first entry)
XX

DE Human beta 1,3-N-acetylglucosamine transferase G4 cDNA sequence.
XX

KM Sugar chain synthesis agent; beta 1,3-N-acetylglucosamine transferase;
XX

KW Inflammation; cancer; metastasis; human; ss.
XX

OS Homo sapiens.
XX

PN MO200100848-A1.
XX

PD 04-JUN-2001.
XX

PF 29-JUN-2000; 2000WC-JP004304.
XX

PR 29-JUN-1999; 99JP-00183437.
XX

PR 16-MAR-2000; 2000JP-00074757.
XX

(KYOW) KYOWA HAKKO KOGYO KK.
XX

Sasaki K, Shiraishi N, Natsune A, Yamada Y, Nakagawa S, Sekine S;
XX

WPI: 2001-102895/11.
XX

P-PSDB; AAB49749.
XX

New polypeptide having beta1,3-N-acetylglucosamine transferase activity
XX

for diagnosis of inflammation, cancer and cancer metastasis, development
XX

of remedies, and for producing glycoconjugates.
XX

Example 3; Fig 1; 195pp; Japanese.
XX

This invention relates to a sugar chain synthesizing agent that contains
XX

a polypeptide as the active ingredient, where the polypeptide has beta
XX

1,3-acetylglucosamine transferase activity. The polypeptides, DNA
XX

sequences encoding them and antibodies directed against the proteins are
XX

useful in the diagnosis of inflammation, cancer and its metastasis,
XX

development of remedies, and for producing sugar chains and
XX

glycoconjugates. Sequences AAB49748 - AAB49751 represent polypeptides of
XX

the invention, having beta 1,3-N-acetylglucosamine transferase activity,
XX

and polynucleotides AAF29255 - AAF29258 represent cDNA encoding them. PCR
XX

|||||
Db 2041 TCAGAGAGCTCCCTACCCAGATATGTTTACAGATTAGAGGGGAGACCGGGTAGCCAGT 2100
Qy 2101 GACCCCTGACAGCCCGCCAGCTTACAGGCTCAGTGTCTGCCAGTCAAGCTTCAAGGCAATT 2160
Db 2101 GACCCCTGACAGCCCGCCAGCTTACAGGCTCAGTGTCTGCCAGTCAAGCTTCAAGGCAATT 2160
Qy 2161 GTGATGGGAGAGCTTGGGGAATATATAATTTGTGAAGCTTGG 2205
Db 2161 GTGATGGGAGAGCTTGGGGAATATATAATTTGTGAAGCTTGG 2205
RESULT 2
ABV22526
ID ABV22526 standard; cDNA; 2427 BP.
AC ABV22526;
DT 13-SBP-2002 (first entry)
XX Human prostate expression marker cDNA 22517.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX WO200160860-A2.
XX 23-AUG-2001;
XX 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183119P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JB;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 3934-3935; 11750bp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 2427 BP; 501 A; 723 C; 655 G; 532 T; 0 U; 16 Other;
Query Match 96.4%; Score 2124.8; DB 5; Length 2427;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 78 GGAGCGCCAGAGAGCTCTCAGCGCAGACCCAGACCTGCTGGCCAGATGAATAT 137
|||||

Db 67 GGAGCGCCAGAGAGCTCTCAGCGCAGACCCAGACCCCTGCTGGCCAGATGAATAT 126
Qy 138 CTCGGGACACGGGAGGCGCAATGCAACCTCATTTGAGGCAATGGGGCTTCAACCTCTC 197
Db 127 CTCGGGACACGGGAGGCGCAATGCAACCTCATTTGAGGCAATGGGGCTTCAACCTCTC 186
Qy 198 CTCCTGAGTCTGCTAGTGTACACCAACCTGCAAGGTCAGAGAGCAACCGGCAATC 257
Db 187 CTCCTGAGTCTGCTAGTGTACACCAACCTGCAAGGTCAGAGAGCAACCGGCAATC 246
Qy 258 CCCGAGCCCTGCTGGCCCACTCCACCAACCGCCAGCCCGCCCGCTGCAATGCC 317
Db 247 CCCGAGCCCTGCTGGCCCACTCCACCAACCGCCAGCCCGCCCGCTGCAATGCC 306
Qy 318 AACACCTATAGTGTACACCAACCGGCACTTCGCAAGGAGCGGAGACGTTGCAATCTC 377
Db 307 AACACCTATAGTGTACACCAACCGGCACTTCGCAAGGAGCGGAGACGTTGCAATCTC 366
Qy 378 CTCCTGAGAGACACTGCGCCCACTTCCCTGCTGCAAGGACGTCGCCCTTAAGTGC 437
Db 367 CTCCTGAGAGACACTGCGCCCACTTCCCTGCTGCAAGGACGTCGCCCTTAAGTGC 426
Qy 438 GCGGACCCGCTTCTCTGCTGCTGTGATCAAGTCTCCCTAGCAACTATGTGCCGCG 497
Db 427 GCGGACCCGCTTCTCTGCTGCTGTGATCAAGTCTCCCTAGCAACTATGTGCCGCG 486
Qy 498 GAGCTGCTCGGGGCACTGTGGGCGCGGAGCGCAAGTACGGGCTTGGACGTGCCCTC 557
Db 487 GAGCTGCTCGGGGCACTGTGGGCGCGGAGCGCAAGTACGGGCTTGGACGTGCCCTC 546
Qy 558 CTCCTTCTGAGGAGCAAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617
Db 547 CTCCTTCTGAGGAGCAAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
Qy 618 GAGCTGAGGAGCAAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677
Db 607 GAGCTGAGGAGCAAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
Qy 678 AACCTCAAGCTCAAGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
Db 667 AACCTCAAGCTCAAGAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
Qy 738 AGCTTCTGCTCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
Db 727 AGCTTCTGCTCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
Qy 798 CTCGAGAGCAATGACCTGCGCGCACTCTTGTGGGGCAACTGATCCAAACGTGGCG 857
Db 787 CTCGAGAGCAATGACCTGCGCGCACTCTTGTGGGGCAACTGATCCAAACGTGGCG 846
Qy 858 CCCATCCGGGCTTTTGGAGCAAGTACTATGTGCCAGAGTGGTACTCAGAAATGAGCGG 917
Db 847 CCCATCCGGGCTTTTGGAGCAAGTACTATGTGCCAGAGTGGTACTCAGAAATGAGCGG 906
Qy 918 TACCCACCTATATGAGGGGGTGGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
Db 907 TACCCACCTATATGAGGGGGTGGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
Qy 978 CGCGTGTGCGCCATGCTTGTGACATCTTCCCATGATGATGATGATGATGATGATGATGAT 1037
Db 967 CGCGTGTGCGCCATGCTTGTGACATCTTCCCATGATGATGATGATGATGATGATGATGAT 1026
Qy 1038 CTGAGAGTTGAGGAGCTGAAGCTGCTGCCACAGGCGCATCGGACGTGTGGCGTGGCG 1097
Db 1027 CTGAGAGTTGAGGAGCTGAAGCTGCTGCCACAGGCGCATCGGACGTGTGGCGTGGCG 1086
Qy 1098 GCTCAGTGGAGACACCTGCTCTCTTGAACCTGCTTCAACGAGACCTGCTGCTGCTGCTG 1157
Db 1087 GCTCAGTGGAGACACCTGCTCTCTTGAACCTGCTTCAACGAGACCTGCTGCTGCTGCTG 1146
Qy 1158 GACCGCTTCTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
Db 1147 GACCGCTTCTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206

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QY 1218 ACCGCGGCATCAGACAGATCTACTGATGACGATCAGGCTCCACCTCTGGGCT 1277
DB 1207 ACCGCGGCATCAGACAGATCTACTGATGACGATCAGGCTCCACCTCTGGGCT 1266
QY 1278 CTTGTTTTCAGAGAGAGAGGCGACACCTTCTCCAGAGAGCTGAGACCTTTGTGCTG 1337
DB 1267 CTTGTTTTCATAGAGAGAGGCGACACCTTCTCCAGAGAGCTGAGACCTTTGTGCTG 1326
QY 1338 AGCATTAAGGAGAGGCGAGAGAGGTTTGTAGTGTGATTAATTTCTGCTGCGGAA 1397
DB 1327 AGCATTAAGGAGAGGCGAGAGAGGTTTGTAGTGTGATTAATTTCTGCTGCGGAA 1386
QY 1398 CTCCTACACATCTCTCAAAACCACTGACTGTTCTCAGACATCTTCCCTGAGTGTGCTG 1457
DB 1387 CTCCTACACATCTCTCAAAACCACTGACTGTTCTCAGACATCTTCCCTGAGTGTGCTG 1446
QY 1458 AGGAACTCCAGAAATATATGATCTTTTGTGCTGCTAATGAGAGAGTGTGCTGCTG 1517
DB 1447 AGGAACTCCAGAAATATATGATCTTTTGTGCTGCTAATGAGAGAGTGTGCTGCTG 1506
QY 1518 TAGAGTTCCAACTGTGAGATGATCCGTCCTGTTGTGATGATTAAGTCTTACTCTGCTGCT 1577
DB 1507 TAGAGTTCCAACTGTGAGATGATCCGTCCTGTTGTGATGATTAAGTCTTACTCTGCTGCT 1566
QY 1578 CACCTACTCAGACGAGATGCTAAGACAGTGCATGCACTGCACTGAGTTAATGAGAGATAGC 1637
DB 1567 CACCTACTCAGACGAGATGCTAAGACAGTGCATGCACTGAGTTAATGAGAGATAGC 1626
QY 1638 TCCGTTCTGAGTTCCAGAGGCGGACGACGAACTCTGTGTCCAAATAGAGTGAAGTGAAGA 1697
DB 1627 TCCGTTCTGAGTTCCAGAGGCGGACGACGAACTCTGTGTCCAAATAGAGTGAAGTGAAGA 1686
QY 1698 ATATCTTTCAGCCAGAGAGAGAGGCTGCTGATCTTAACCTTCTGCTGCTGCTGACAA 1757
DB 1687 ATATCTTTCAGCCAGAGAGAGAGGCTGCTGATCTTAACCTTCTGCTGCTGCTGACAA 1746
QY 1758 CTCAGAGGTTGGGGGATACAGAGAGTGTGTGATAGACCCGCTCTCTTACTTG 1817
DB 1747 CTCAGAGGTTGGGGGATACAGAGAGTGTGTGATAGACCCGCTCTCTTACTTG 1806
QY 1818 TGGGATCAATCTGTATATGTGTGAGTGTGCGCAGAGAGAGGAGCAAGTCTTTGAA 1877
DB 1807 TGGGATCAATCTGTATATGTGTGAGTGTGCGCAGAGAGAGGAGCAAGTCTTTGAA 1866
QY 1878 AGTTGTGAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGCCGCCATCCCTGTGTTCC 1937
DB 1867 AGTTGTGAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGCCGCCATCCCTGTGTTCC 1926
QY 1938 AAGATTTCAGAGAACAGCACTGGGGCTGGAATGATCTTTAATGAGCCCAAGGCCAAACAG 1997
DB 1927 AAGATTTCAGAGAACAGCACTGGGGCTGGAATGATCTTTAATGAGCCCAAGGCCAAACAG 1986
QY 1998 CATATGCTCTCATCTAGCTGTGAGAGAGGAGATTCAGGCTCCACAGCTCTCCCTCA 2057
DB 1987 CATATGCTCTCATCTAGCTGTGAGAGAGGAGATTCAGGCTCTCCACAGCTCTCCCTCA 2046
QY 2058 CCCAGATGTTTTCAGATTAAGAGGAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2117
DB 2047 CCCAGATGTTTTCAGATTAAGAGGAGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2106
QY 2118 AGCTTCAGAGCTCTCATGCTGTGCAATCAAGCTTCAAGAGCATTTGTATGAGGAGGAGCTTGG 2177
DB 2107 AGCTTCAGAGCTCTCATGCTGTGCAATCAAGCTTCAAGAGCATTTGTATGAGGAGGAGCTTGG 2166
QY 2178 GGAATATATATATTTTGTGAAGACTTGG 2205
DB 2167 GGAATATATATATTTTGTGAAGACTTGG 2194
```

RESULT 3
ABV28341
ID ABV28341 standard; cDNA; 2427 BP.

```
XX AC ABV28341;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker CDNA 28332.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN MO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PS Claim 1; Page 5904; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX SO Sequence 2427 BP; 501 A; 723 C; 655 G; 532 T; 0 U; 16 Other;
Query Match 96.4%; Score 2124.8; DB 5; Length 2427;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2126; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 78 GGAAGCGCCAGAGAGGCTCTCTCAGGCGGAGCCCGAGACCTTGCTGCGCAGAGATGAT 137
DB 67 GGAAGCGCCAGAGAGGCTCTCTCAGGCGGAGCCCGAGACCTTGCTGCGCAGAGATGAT 126
QY 138 CTCGCGACCGGAGGCGCCATGACCTCATCTTGTGGCATCGGCGCTTTCACCTCTCTC 197
DB 127 CTCGCGACCGGAGGCGCCATGACCTCATCTTGTGGCATCGGCGCTTTCACCTCTCTC 186
QY 198 CTCCTTCACTGTTAGTGTACCAACCACTGCAAGTGTCAAGAGAGCAGCCGCGGATC 257
DB 187 CTCCTTCACTGTTAGTGTACCAACCACTGCAAGTGTCAAGAGAGCAGCCGCGGATC 246
QY 258 CCGAGAGCCCTGCGCTGCGGCACTTCAGACCAACCGGCGGAGCCCGGCGGCGGATGCG 317
DB 247 CCGAGAGCCCTGCGCTGCGGCACTTCAGACCAACCGGCGGAGCCCGGCGGCGGATGCG 306
QY 318 AACACCTTATGTGTACCAACCGGACTTGTGCGCAGCAGCCGCGAGCAGTTCAGAACTTC 377
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Db 307 AACACCTATGATGATCAACCAACCCGACCTTCCGACCAACGCGACAGACGTTACGAACCTTC 366
Qy 378 CTCCTGTACAGACACTGCGCCGCACTTTCCCTGCTGAGGACGTGCCCCCTCTAAATGTC 437
Db 367 CTCCTGTACAGACACTGCGCCGCACTTTCCCTGCTGAGGACGTGCCCCCTCTAAATGTC 426
Qy 438 GCGACACCGGTCCTTCTGCTGCTGATGATCAAGTCCCTCCCTAGCAACTATATGCGCCGC 497
Db 427 GCGACACCGGTCCTTCTGCTGCTGATGATCAAGTCCCTCCCTAGCAACTATATGCGCCGC 486
Qy 498 GAGCTGCTCGGCGCACTGCGGCGCGAGCGGCAAGGTAAGGCTTTGACATGCGCTC 557
Db 487 GAGCTGCTCGGCGCACTGCGGCGCGAGCGGCAAGGTAAGGCTTTGACATGCGCTC 546
Qy 558 CTCCTGCTGCTGCGGCACTGCGGCGCGAGCGGCAAGGTAAGGCTTTGACATGCGCTC 617
Db 547 CTCCTGCTGCTGCGGCACTGCGGCGCGAGCGGCAAGGTAAGGCTTTGACATGCGCTC 606
Qy 618 GAGCTGAGGCAACAGACTCAACGAGACATCTGCTGAGGGAATTTCCAGCATCTCTTCTTC 677
Db 607 GAGCTGAGGCAACAGACTCAACGAGACATCTGCTGAGGGAATTTCCAGCATCTCTTCTTC 666
Qy 678 AACCTCAGGCTCAAGAGGTCCTGTTCTTACAGTGGGAGGACAAAGTGCAGCAAGCC 737
Db 667 AACCTCAGGCTCAAGAGGTCCTGTTCTTACAGTGGGAGGACAAAGTGCAGCAAGCC 726
Qy 738 AGCTTGCTGCTCAACGCGGATGATGACGTTTGGACACACAGACAAATGCTTCTTAC 797
Db 727 AGCTTGCTGCTCAACGCGGATGATGACGTTTGGACACACAGACAAATGCTTCTTAC 786
Qy 798 CTGCAAGACCAATCACTTGGCGCCGCACTTCTGCTGCGGCACTGATCCAAACGTCGCG 857
Db 787 CTGCAAGACCAATCACTTGGCGCCGCACTTCTGCTGCGGCACTGATCCAAACGTCGCG 846
Qy 858 CCCATCCGCGGCTTTTGGAGCAAGTACTATGTCGCAAGGTCGATCTCAAGATGAGCG 917
Db 847 CCCATCCGCGGCTTTTGGAGCAAGTACTATGTCGCAAGGTCGATCTCAAGATGAGCG 906
Qy 918 TACCCACCTTATTTGGGGGTGGTGGCTTCTGCTGCTCCGCTTCAACGCGCTGCTGC 977
Db 907 TACCCACCTTATTTGGGGGTGGTGGCTTCTGCTGCTCCGCTTCAACGCGCTGCTGC 966
Qy 978 CGCGGTGCTGCCATATCTTGGACATCTTCCCATTTGATGATGCTTCCGCGGTATGCT 1037
Db 967 CGCGGTGCTGCCATATCTTGGACATCTTCCCATTTGATGATGCTTCCGCGGTATGCT 1026
Qy 1038 CTGGAAGCTTGAAGGAGCTGAAGCTGCTCCACAGCGGCACTCCGCAAGTTCGCGG 1097
Db 1027 CTGGAAGCTTGAAGGAGCTGAAGCTGCTCCACAGCGGCACTCCGCAAGTTCGCGG 1086
Qy 1098 GCTCATCGCAACACCTGCTCTCTTGGACCTTGTCTTCAACGAGACGTCGTCGTC 1157
Db 1087 GCTCATCGCAACACCTGCTCTCTTGGACCTTGTCTTCAACGAGACGTCGTCGTC 1146
Qy 1158 CACCGCTTCTTACCTTATGATGATGCTGCTATATGAGGATGCGCTGAACAGCCCACTTC 1217
Db 1147 CACCGCTTCTTACCTTATGATGATGCTGCTATATGAGGATGCGCTGAACAGCCCACTTC 1206
Qy 1218 ACCTGCGGCAATGAGACAGATCTACTGATGAGCATGAGGATCCCAAGCTCTGAGGCT 1277
Db 1207 ACCTGCGGCAATGAGACAGATCTACTGATGAGCATGAGGATCCCAAGCTCTGAGGCT 1266
Qy 1278 CCGTGTTCAGAGAAAGGCGGCAACCTTCTCTCCAGGAAGCTGAGACCTTTGTCGTC 1337
Db 1267 CCGTGTTCAGAGAAAGGCGGCAACCTTCTCTCCAGGAAGCTGAGACCTTTGTCGTC 1326
Qy 1338 AGCATTAAGGAGAGTCCAGGGAAGTTTGAGGTTGATGATGAATATCTTGGCTGCGGAA 1397
Db 1327 AGCATTAAGGAGAGTCCAGGGAAGTTTGAGGTTGATGATGAATATCTTGGCTGCGGAA 1386
Qy 1398 CTCCTACATCTCTTCAAAACCAACCTGATGCTTCCAGCATCTTCCCTGATGTCGTCG 1457

Db 1387 CTCCTACATCTCTTCAAAACCAACCTGATGCTTCCAGCATCTTCCCTGATGTCGTCG 1446
Qy 1458 AGGAACTCCAGAAATAATGATCTTTTGTGGCTGCTAATGCGAAGATGCTGTCG 1517
Db 1447 AGGAACTCCAGAAATAATGATCTTTTGTGGCTGCTAATGCGAAGATGCTGTCG 1506
Qy 1518 TAGAGTTCCAACTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1577
Db 1507 TAGAGTTCCAACTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
Qy 1578 CACCTACTCAACAGCGGATGCTAAGCAGTGACCTGCACTGCTGCTTAAATGCGATATAGC 1637
Db 1567 CACCTACTCAACAGCGGATGCTAAGCAGTGACCTGCACTGCTGCTTAAATGCGATATAGC 1626
Qy 1638 TCCGTCGAGTTCAGGCGCCAGCAAACTCTGTCGCTCAATAGCTGAGCTGAGGAA 1697
Db 1627 TCCGTCGAGTTCAGGCGCCAGCAAACTCTGTCGCTCAATAGCTGAGCTGAGGAA 1686
Qy 1698 ATATCTTTCAGCCAGGAGAGGAGGCTGCTGATCTTAACTCTTCTGCTGCTCAGACAA 1757
Db 1687 ATATCTTTCAGCCAGGAGAGGAGGCTGCTGATCTTAACTCTTCTGCTGCTCAGACAA 1746
Qy 1758 CTCAGAAAGTGGGAGGATACAGAGAGTGTGGAATAGACCGCCCTCTTACTTG 1817
Db 1747 CTCAGAAAGTGGGAGGATACAGAGAGTGTGGAATAGACCGCCCTCTTACTTG 1806
Qy 1818 TGGGATCAAAATGCTGTAATGCTGAGAGTGTGGGCAAGAGGAGGCAATGCTTTGAA 1877
Db 1807 TGGGATCAAAATGCTGTAATGCTGAGAGTGTGGGCAAGAGGAGGCAATGCTTTGAA 1866
Qy 1878 AGTTGAGAGGCTCAGAGTTTCTGAGGCTCTCATTAAGGAGCCCAATCCCTGATTCGC 1937
Db 1867 AGTTGAGAGGCTCAGAGTTTCTGAGGCTCTCATTAAGGAGCCCAATCCCTGATTCGC 1926
Qy 1938 AAGAAATTCAGAGAACAGCACTGGGCTGGAATATCTTAAATGAGGCCCAACAGG 1997
Db 1927 AAGAAATTCAGAGAACAGCACTGGGCTGGAATATCTTAAATGAGGCCCAACAGG 1986
Qy 1998 CATATGCTTCACTATGCTGCTGAGAAAGGAGAAATTCAGGTCCTCCAGCAGCTCTCTCA 2057
Db 1987 CATATGCTTCACTATGCTGCTGAGAAAGGAGAAATTCAGGTCCTCCAGCAGCTCTCTCA 2046
Qy 2058 CCCAGTATGTTTAAAGATTAAGAGGAGGAGCCGAGTGAAGCAGGAGCCCTGAGCCCC 2117
Db 2047 CCCAGTATGTTTAAAGATTAAGAGGAGGAGCCGAGTGAAGCAGGAGCCCTGAGCCCC 2106
Qy 2118 AGCTTCAAGGCTCAGTGTCTGCAATCAAGCTTCAAGGATTTGATGAGGAGCCTTG 2177
Db 2107 AGCTTCAAGGCTCAGTGTCTGCAATCAAGCTTCAAGGATTTGATGAGGAGCCTTG 2166
Qy 2178 GGGAAATTAATAATTTTGTGAAGCTTGG 2205
Db 2167 GGGAAATTAATAATTTTGTGAAGCTTGG 2194

RESULT 4
AAS46068
ID AAS46068 standard; cDNA; 2210 BP.
XX
XX AAS46068;
XX
XX
XX Human DNA encoding PRO polypeptide sequence #144.
XX
XX PRO polypeptide: mammal; tumour; cancer; human; cattle; horse; sheep; 88;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
XX PCR primer.
XX
XX Homo sapiens.
XX OS

EN WO20016848-A2.
 XX 20-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006520.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 03-MAR-2000; 2000US-018702P.
 XX 06-MAR-2000; 2000US-0186968P.
 XX 14-MAR-2000; 2000US-0189328P.
 XX 14-MAR-2000; 2000US-0189328P.
 XX 15-MAR-2000; 2000US-0190884P.
 XX 21-MAR-2000; 2000US-0190828P.
 XX 21-MAR-2000; 2000US-0191007P.
 XX 21-MAR-2000; 2000US-0191048P.
 XX 28-MAR-2000; 2000US-0192655P.
 XX 29-MAR-2000; 2000US-0193032P.
 XX 29-MAR-2000; 2000US-0193053P.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 04-APR-2000; 2000US-0194449P.
 XX 11-APR-2000; 2000US-0195975P.
 XX 11-APR-2000; 2000US-0196000P.
 XX 11-APR-2000; 2000US-0196187P.
 XX 11-APR-2000; 2000US-0196690P.
 XX 18-APR-2000; 2000US-0198121P.
 XX 18-APR-2000; 2000US-0198585P.
 XX 25-APR-2000; 2000US-0199397P.
 XX 25-APR-2000; 2000US-0199550P.
 XX 03-MAY-2000; 2000US-0196549P.
 XX 17-MAY-2000; 2000WO-US013705.
 XX 22-MAY-2000; 2000WO-US014042.
 XX 30-MAY-2000; 2000WO-US014941.
 XX 02-JUN-2000; 2000WO-US015264.
 XX 05-JUN-2000; 2000US-0209832P.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 22-AUG-2000; 2000US-00644848.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 08-NOV-2000; 2000WO-US030952.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000WO-US034956.
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-602746/68.
 DR P-PSDB; AAU29167.
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 2; Fig 287; 774pp; English.
 CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumor in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumor in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumor necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,

CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 CC
 XX
 SQ Sequence 2210 BP; 467 A; 672 C; 603 G; 468 T; 0 U; 0 Other;
 Query Match 96.1%; Score 2119.8; DB 4; Length 2210;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 78 GGAGCCGCGCAGAGAGCTCTCAGGCGAGCCGAGACCTGTGCGCCAGATGAAGTAT 137
 Db GGAAGCCGCGCAGAGAGCTCTCAGGCGAGCCGAGACCTGTGCGCCAGATGAAGTAT 111
 QY CTCGCGCACCGGCGGCGCAATGCCACCTCAATTCGTGCGCATGCGGCTTTCACCTCCTC 197
 Db CTCGCGCACCGGCGGCGCAATGCCACCTCAATTCGTGCGCATGCGGCTTTCACCTCCTC 171
 QY CTCCTCAGTCGTGATGTCACACCCACCTGCAAGGTCCAGAGCAGCCAGCGGATC 257
 Db CTCCTCAGTCGTGATGTCACACCCACCTGCAAGGTCCAGAGCAGCCAGCGGATC 231
 QY CCGGAGGCGCTGAGCTGAGCCCACTCCACCCAGCCGCGGCGCGGCGGCGGATGCGC 317
 Db CCGGAGGCGCTGAGCTGAGCCCACTCCACCCAGCCGCGGCGCGGCGGCGGATGCGC 291
 QY AACACCTTATGTCACCCACCGGACTTGCGCCAGCGGCGGCGGATGCGC 377
 Db AACACCTTATGTCACCCACCGGACTTGCGCCAGCGGCGGCGGATGCGC 351
 QY CTCCTGTCACAGACATGCGCGCACTTCCCTGTCGAGAGACGCGGCGGCGGATGCGC 437
 Db CTCCTGTCACAGACATGCGCGCACTTCCCTGTCGAGAGACGCGGCGGCGGATGCGC 411
 QY GCGGAGCGGCTCTTCTGTCGTGATGATCAAGTCTCCCTGACATGATGTCGCGCGC 497
 Db GCGGAGCGGCTCTTCTGTCGTGATGATCAAGTCTCCCTGACATGATGTCGCGCGC 471
 QY GAGCTGCTGCGGCGCAGTGGGCGCGGAGCGGAGGATGAGGCGGCTTTCAGCTGCGCTC 557
 Db GAGCTGCTGCGGCGCAGTGGGCGCGGAGCGGAGGATGAGGCGGCTTTCAGCTGCGCTC 531
 QY CTCTTCTGCTGAGGCGCAGGCTCCCAACCGGCGGCGGCGGCGGCGGATGCGC 617
 Db CTCTTCTGCTGAGGCGCAGGCTCCCAACCGGCGGCGGCGGCGGCGGATGCGC 591
 QY GAGCTGAGGCGACAGACTCAAGGACATCTGCAAGTGGGACTTCCAGCATCTCTTCTTC 677
 Db GAGCTGAGGCGACAGACTCAAGGACATCTGCAAGTGGGACTTCCAGCATCTCTTCTTC 651
 QY AACCTCAGCTCAAGAGGCTCTTCTTACAGTGCAGAGACAGAGGCGGCGGCGGCGC 737
 Db AACCTCAGCTCAAGAGGCTCTTCTTACAGTGCAGAGACAGAGGCGGCGGCGGCGC 711
 QY AGCTTGTGCTCAAGCGGAGATGACGCTTTCACACAGACAGACATGCTTCTTAC 797
 Db AGCTTGTGCTCAAGCGGAGATGACGCTTTCACACAGACAGACATGCTTCTTAC 771
 QY CTGCAAGACATAGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 857
 Db CTGCAAGACATAGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 831
 QY CCGATCCGCGGCTTTCAGAGCAAGTATGTCAGAGAGGCTGATCAGAAATGAGCGG 917
 Db CCGATCCGCGGCTTTCAGAGCAAGTATGTCAGAGAGGCTGATCAGAAATGAGCGG 891
 QY TACCCACCTTATGTCAGAGGCTGCTTTCAGAGGCTGCTTTCAGAGGCTGCTTTCAG 977
 Db TACCCACCTTATGTCAGAGGCTGCTTTCAGAGGCTGCTTTCAGAGGCTGCTTTCAG 951
 QY CCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1037
 Db CCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1011

Oy	1038	CTGGAGCTTGAAGGAGCTGAAGCTGCGCTCCCAAGCGGCAATCCGAGCTGCGGGGTGGG	1097
Db	1012	CTGGAGCTTGAAGGAGCTGAAGCTGCGCTCCCAAGCGGCAATCCGAGCTGCGGGGTGGG	1071
Oy	1098	GCTCCATGCAACACTGTCTCTCTTTGACCCCTGTCTTACCGAGACTTGTCTGTGGT	1157
Db	1072	GCTCCATGCAACACTGTCTCTCTTTGACCCCTGTCTTACCGAGACTTGTCTGTGGT	1131
Oy	1158	CACCGCTTCTTACCTTATGAGATGTGCTCATGTGGATGCGCTGAACCAAGCCCACTC	1217
Db	1132	CACCGCTTCTTACCTTATGAGATGTGCTCATGTGGATGCGCTGAACCAAGCCCACTC	1191
Oy	1218	ACCTGGCGGCATTCAGACACAGATCTACTGAGTCAGACATCAGGGTCTCCAGCTCTGGGCT	1277
Db	1192	ACCTGGCGGCATTCAGACACAGATCTACTGAGTCAGACATCAGGGTCTCCAGCTCTGGGCT	1251
Oy	1278	CCTGTTTCCAGAGAAAGGGGGGACACCTTCTCTCCAGAGACTGAGACTTGTGTGCTG	1337
Db	1252	CCTGTTTCCAGAGAAAGGGGGGACACCTTCTCTCCAGAGACTGAGACTTGTGTGCTG	1311
Oy	1338	AGCATTAAGGAGTGCAGAGGAAGTTTGAGGTTTGATGATGAAATATTCTGGCTGCGAA	1397
Db	1312	AGCATTAAGGAGTGCAGAGGAAGTTTGAGGTTTGATGATGAAATATTCTGGCTGCGAA	1371
Oy	1388	CTCTTACACATCTTTCAAAACCACCTGTGATCTGTTCCAGACTTCTCCCTGGATGGCTGG	1457
Db	1372	CTCTTACACATCTTTCAAAACCACCTGTGATCTGTTCCAGACTTCTCCCTGGATGGCTGG	1431
Oy	1458	AGGAATCTCAAAAATATGATCTTTCTTTTGTGGCTGTATATGGAGAAATGTGCTGTGC	1517
Db	1432	AGGAATCTCAAAAATATGATCTTTCTTTTGTGGCTGTATATGGAGAAATGTGCTGTGC	1491
Oy	1518	TAGAGTTTCCAATGTGATGTGATCCGTGCCCTTTGAGTCAAAAGTCTTACTTCCCTGTCT	1577
Db	1492	TAGAGTTTCCAATGTGATGTGATCCGTGCCCTTTGAGTCAAAAGTCTTACTTCCCTGTCT	1551
Oy	1578	CACCTACTCAGACAGCGGAGTCTTAAGCAGTGCACCTGAGTGTTTATATGGCAGATTAAGC	1637
Db	1552	CACCTACTCAGACAGCGGAGTCTTAAGCAGTGCACCTGAGTGTTTATATGGCAGATTAAGC	1611
Oy	1638	TCCGTCTGCAATTCAGAGCCAGGCCAGAAATCTCTGTGTCCCATATAGACTGACGTGAGAA	1697
Db	1612	TCCGTCTGCAATTCAGAGCCAGGCCAGAAATCTCTGTGTCCCATATAGACTGACGTGAGAA	1671
Oy	1698	ATATCTTTCAAGCCAGGAGAGAGGGGTCTGATCTTTAACCCCTTCTCGGGTCTCAGACAA	1757
Db	1672	ATATCTTTCAAGCCAGGAGAGAGGGGTCTGATCTTTAACCCCTTCTCGGGTCTCAGACAA	1731
Oy	1758	CTCAGAAAGTTGGGGGGGATACAGAGAGTGTGGAATATAGACCGCCCTCTTACTTG	1817
Db	1732	CTCAGAAAGTTGGGGGGGATACAGAGAGTGTGGAATATAGACCGCCCTCTTACTTG	1791
Oy	1818	TGGGATCAAAATGCTGTATATGGTGAAGGTGTGGGACAGAGAGAGGCAAGTCTTTGAA	1877
Db	1792	TGGGATCAAAATGCTGTATATGGTGAAGGTGTGGGACAGAGAGAGGCAAGTCTTTGAA	1851
Oy	1878	AGTTGTGAGACTCAGAGTTTCTTGGGGTCTCATTTAGAGGCCCAATCCCTGTGTCTCCC	1937
Db	1852	AGTTGTGAGACTCAGAGTTTCTTGGGGTCTCATTTAGAGGCCCAATCCCTGTGTCTCCC	1911
Oy	1938	AAGAATTCAGAGAACAGACTGCGGGCTGGAATGTATCTTTAATGGGCCAAGGCAACAGG	1997
Db	1912	AAGAATTCAGAGAACAGACTGCGGGCTGGAATGTATCTTTAATGGGCCAAGGCAACAGG	1971
Oy	1998	CATAATGCTCTATCTGCTTGAGAAAGGAGATTCAGTGTCTTCAGACAGCTTCCCTCA	2057
Db	1972	CATAATGCTCTATCTGCTTGAGAAAGGAGATTCAGTGTCTTCAGACAGCTTCCCTCA	2031
Oy	2058	CCCGATATGTTTATCAGATTTACGGGGGGGACCGGGGTAGCCAGATGACCCCTCTGACGCCCC	2117
Db	2032	CCCGATATGTTTATCAGATTTACGGGGGGGACCGGGGTAGCCAGATGACCCCTCTGACGCCCC	2091

Qy	2118	AGCTTCAGGCTCAGTGTCCAGTCACAGCTGATGGGCGCCTTG	2117
Db	2092	AGCTTCAGGCTCAGTGTCTCCAGTCACAGCTTGTATGGGCGCCTTG	2151
Qy	2178	GGGAATATAAAATTTTGTGAAGA	2200
Db	2152	GGGAATATAAAATTTTGTGAAGA	2174
RESULT 5			
ID	ABX78671	standard; cDNA; 2210 BP.	
XX	ABX78671;		
AC	15-APR-2003	(first entry)	
DT	Human PRO polynucleotide #144.		
DE	Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;		
KW	liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;		
KW	antibody-dependent enzyme mediated produg therapy.		
XX	Homo sapiens.		
XX	US2003027272-A1.		
XX	06-FEB-2003.		
XX	21-JUN-2002; 2002US-00176492.		
PF	18-SEP-1997;	97US-0059263P.	
PR	18-SEP-1997;	97US-0059266P.	
PR	17-OCT-1997;	97US-0062250P.	
PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0063120P.	
PR	24-OCT-1997;	97US-0063121P.	
PR	28-OCT-1997;	97US-0063540P.	
PR	28-OCT-1997;	97US-0063541P.	
PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063564P.	
PR	29-OCT-1997;	97US-0063734P.	
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PR	31-OCT-1997;	97US-0064103P.	
PR	13-NOV-1997;	97US-0065311P.	
PR	21-NOV-1997;	97US-0066120P.	
PR	24-NOV-1997;	97US-0066466P.	
PR	24-NOV-1997;	97US-0066772P.	
PR	11-DEC-1997;	97US-0069335P.	
PR	12-DEC-1997;	97US-0069425P.	
PR	17-DEC-1997;	97US-0069870P.	
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PR	10-MAR-1998;	98US-0077450P.	
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PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083498P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
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PR 16-SEP-1998; 98US-0100664P.
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PR 29-SEP-1998; 98US-0102330P.
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PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 96.1%; Score 2119.8; DB 7; length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 78 GGAGCCGCCGAGAGGCTCTTCAGGCCAGACCCGAGACCCCTGTGGCCAGATGAATAT 137
Db 52 GGAGCCGCCGAGAGGCTCTTCAGGCCAGACCCGAGACCCCTGTGGCCAGATGAATAT 111

QY 138 CTCGGGACCGGGGCGCAATGCGACCCCTCATTTGGGCGATCGGCGCTTTCACCCCTCTC 197
DB 112 CTCGGGACCGGGGCGCAATGCGACCCCTCATTTGGGCGATCGGCGCTTTCACCCCTCTC 171
QY 198 CTCCTAGTCTGTAGTGTACCAACCACTGCAAGGTCCAGAGCAGCCAGCGGATC 257
DB 172 CTCCTAGTCTGTAGTGTACCAACCACTGCAAGGTCCAGAGCAGCCAGCGGATC 231
QY 258 CCCGAAGCCCTGGCCCTGGCCCACTCCACCCCGCCAGCCCGGCGCCCTGTCATGCC 317
DB 232 CCCGAAGCCCTGGCCCTGGCCCACTCCACCCCGCCAGCCCGGCGCCCTGTCATGCC 291
QY 318 AACACCTATGTGTACCCGACCCGGAATTGCGACGCGGAGCGAGCGTTGAGAACTTC 377
DB 292 AACACCTATGTGTACCCGACCCGGAATTGCGACGCGGAGCGAGCGTTGAGAACTTC 351
QY 378 CTCCTGTACAGACATGCGCGCACTTCCCTGTGCGAGACGTGCCCCCTTAAGTGC 437
DB 352 CTCCTGTACAGACATGCGCGCACTTCCCTGTGCGAGACGTGCCCCCTTAAGTGC 411
QY 438 GCGGACCGGCTCTTCTGTGCTGTGTATGAATCCTCCCTTAGCACTATGTGCGCGC 497
DB 412 GCGGACCGGCTCTTCTGTGCTGTGTATGAATCCTCCCTTAGCACTATGTGCGCGC 471
QY 498 GAGCTGCTGGGCGCACTGTGGGCGCGGAGCGGAGGTAGGGGTTTGCAGTGGCGCTC 557
DB 472 GAGCTGCTGGGCGCACTGTGGGCGCGGAGCGGAGGTAGGGGTTTGCAGTGGCGCTC 531
QY 558 CTCCTTCTGTGTGGCAAGCTTCAACCCGCAAGAGCCCGCAAGGTCAACCGGCTGCTG 617
DB 532 CTCCTTCTGTGTGGCAAGCTTCAACCCGCAAGAGCCCGCAAGGTCAACCGGCTGCTG 591
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DT 07-JUN-2003 (first entry)
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
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OS      Homo sapiens.
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Best local similarity 95.56; P-rod. NO. 0;
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QY	138	CTCGGAGCAGCGGCGGCGCCAAATGCAACCTCATTTGCGCATGAGCGCTTTCACCTCTCTC	197
Db	112	CTCGGAGCAGCGGCGGCGCCAAATGCAACCTCATTTGCGCATGAGCGCTTTCACCTCTCTC	171
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Db	592	GAGCTGAGGCAAGACTTCACGAGACATCTGCAAGTGGGACTTCACAGCTCTTCTTC	651
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11-AUG-2003 (first entry)

Novel human secreted and transmembrane protein PRO1266 cDNA.

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KW affinity purification; gene.
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PR	06-OCT-1998	98US-0103449
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KW knockout; chromosome identification; tissue typing; tumour;
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KW tumour necrosis factor-alpha release stimulator; gene; ss.
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XX ACA93926;
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DT 18-JUL-2003 (first entry)
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KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KM proliferation; differentiation; chondrocyte cell; TNF-alpha;
XX tumour necrosis factor-alpha; gene therapy.
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PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00187746.
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PR

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QY	198	CTCTTCAGTCTGCTAGTGTCAACAACCCGACTGCAAGGTCCAGAGCACCAACCGGCAATC	257
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QY	258	CCCGAGGCCCTTGAGCTTGAGCCCACTCAACCAACCGGCCAGCCCGGACCCTGCGCATCC	317
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QY	498	GAGGTGTGCGGCGCAGTGGGGGCGGACGAGGCAAGGATCGGGGTTTCACTGCGCTC	557
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QY	678	AACTCAACGCTCAAGCAGTCTCTTCTTACAGTGGCAGAGACAAGGTGCGCAACGCC	737
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Dp	1072	GCTTCATGCAACACCTGTCTCTCTTTGACCCCTGCTTCTACCGAGACTGTGCTGTG	1131
QY	1158	CACCGCTTCCATCCTTTATGAGATGCTGCTCATATGTTGGATGCGCTGAAACAGCCCAATCTC	1217
Dp	1132	CACCGCTTCCATCCTTTATGAGATGCTGCTCATATGTTGGATGCGCTGAAACAGCCCAATCTC	1191
QY	1218	ACCTGCGGCAATCAGACACAGATCTAATGATGATGATCAGAGGTCCCGACGCTCTGGAGCT	1277
Dp	1192	ACCTGCGGCAATCAGACACAGATCTAATGATGATGATCAGAGGTCCCGACGCTCTGGAGCT	1251
QY	1278	CTGTGTTTCAAGAGGAAGGGGCGACACCTTCTCTCCAGAGAAAGCTGAGACTTTGTGTGCTG	1337
Dp	1252	CTGTGTTTCAATAGGAAGGGGCGACACCTTCTCTCCAGAGAAAGCTGAGACTTTGTGTGCTG	1311
QY	1338	AGCATTAAGGAGATGCCAGGGAAGGTTTGAAGTTTGAATGATGATTAATTTCTGAGCTGGGAA	1397
Dp	1312	AGCATTAAGGAGATGCCAGGGAAGGTTTGAAGTTTGAATGATGATTAATTTCTGAGCTGGGAA	1371
QY	1398	CTCCTTAACATCTCTTCAAAACCCACCTGATATCTGTTCCAGATCTTCCCTGGATGGCTGG	1457
Dp	1372	CTCCTTAACATCTCTTCAAAACCCACCTGATATCTGTTCCAGATCTTCCCTGGATGGCTGG	1431
QY	1458	AGGAACCTCAAGAAATAATGATCTTCTTTTGTGTGCTCTAATGACAGAAAGTGTGCTGTG	1517
Dp	1432	AGGAACCTCAAGAAATAATGATCTTCTTTTGTGTGCTCTAATGACAGAAAGTGTGCTGTG	1491
QY	1518	TAGAGTTCCAACTGTGATGATCTGCTGCTGGTTTGAATCAAAAGCTTTACTTCTCTGCTCT	1577
Dp	1492	TAGAGTTCCAACTGTGATGATCTGCTGCTGGTTTGAATCAAAAGCTTTACTTCTCTGCTCT	1551
QY	1578	CACCTACTCAAGACGGGATGCTTAAGAGATGACACTGACAGTGGTTTAATGGCAGATTAAGC	1637
Dp	1552	CACCTACTCAAGACGGGATGCTTAAGAGATGACACTGACAGTGGTTTAATGGCAGATTAAGC	1611
QY	1638	TCCGTTCTGAGATTCCAGGCGAGCCAGAGAACTCTGTGTTCACAATAGACTGACGTGAGAA	1697
Dp	1612	TCCGTTCTGAGATTCCAGGCGAGCCAGAGAACTCTGTGTTCACAATAGACTGACGTGAGAA	1671
QY	1698	ATATCTTTCAAGCCAGAGAGAGAGGAGTCTGATCTTAACTCTTCTCTGGTCTTCAGACAA	1757
Dp	1672	ATATCTTTCAAGCCAGAGAGAGAGAGGAGTCTGATCTTAACTCTTCTCTGGTCTTCAGACAA	1731
QY	1758	CTCAGAAAGTTTGGGGGGATACACAGAGAGGTGTGGAAATAGAACCGGCCCTCCTTACTTG	1817
Dp	1732	CTCAGAAAGTTTGGGGGGATACACAGAGAGGTGTGGAAATAGAACCGGCCCTCCTTACTTG	1791
QY	1818	TGGATCAAAATGCTGTATGTGTGAGGTGTGGGACAGAGAGGAGCAATGTCTTTGAA	1877
Dp	1792	TGGATCAAAATGCTGTATGTGTGAGGTGTGGGACAGAGAGGAGCAATGTCTTTGAA	1851
QY	1878	AGTTGTGAGAGCTCAGAGTTTCTGGGGTCTCTAATTAGAGACCCCATCTCTGTGTCTCC	1937
Dp	1852	AGTTGTGAGAGCTCAGAGTTTCTGGGGTCTCTAATTAGAGACCCCATCTCTGTGTCTCC	1911
QY	1938	AAGAAATTCAAGAAACAGCACTGGGGCTGGAAATGATCTTTAAATGGGCCAAGGCCAACAGG	1997
Dp	1912	AAGAAATTCAAGAAACAGCACTGGGGCTGGAAATGATCTTTAAATGGGCCAAGGCCAACAGG	1971
QY	1998	CATATGCTCACTACTGCTCGAGAAAGGAGATTCAGGTCTCTCAGACAGCTCTCCCTCA	2057
Dp	1972	CATATGCTCACTACTGCTCGAGAAAGGAGATTCAGGTCTCTCAGACAGCTCTCCCTCA	2031
QY	2058	CCCAATATGTTTTCACAGATTAAGGGGGAGACGGAGTGAGCCAGTGAACCCCTCGACAGCCCC	2117

Db	2032	CCCATATGTTTACAGATTACGGGGGACCGGGTGAGCCAGTACCCTGCAAGCCCC	2091
Qy	2118	AGCTTCAGGCTCTAGTGTCTGCCAGTCAAGCTTCAACAGGCATTGTGATGGGCGAGCCTTG	2177
Db	2092	AGCTTCAGGCTCTAGTGTCTGCCAGTCAAGCTTCAACAGGCATTGTGATGGGCGAGCCTTG	2151
Qy	2178	GGGATATATAAATTTGTGAAGA	2200
Db	2152	GGGATATATAAATTTGTGAAGA	2174

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Job time : 864 secs

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OM nucleic - nucleic search, using sw model

Run on: June 14, 2004, 10:06:10 ; Search time 160 Seconds

(without alignments)
7647.917 Million cell updates/sec

Title: US-10-019-735-6

Perfect score: 2205

Sequence: 1 ggcacgaagcagccgcaagcg.....aaattctgtgaacttg 2205

Scoring table: IDENTITY NUC

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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	188.4	8.5	1420	4 US-09-482-180A-1	Sequence 1, Appl
2	180.8	8.2	1134	4 US-09-482-180A-3	Sequence 3, Appl
3	102.2	4.6	1191	4 US-09-459-133-3	Sequence 3, Appl
4	94.4	4.3	1532	4 US-09-459-133-1	Sequence 1, Appl
5	81.8	3.7	1167	4 US-09-459-133-14	Sequence 12, Appl
6	77.8	3.5	1446	4 US-09-459-133-12	Sequence 14, Appl
7	74.2	3.4	1434	4 US-09-055-097-2	Sequence 2, Appl
8	74.2	3.4	1434	4 US-09-373-902-2	Sequence 2, Appl
9	59.8	2.7	7218	1 US-08-232-463-14	Sequence 14, Appl
10	55.6	2.5	1926	4 US-09-249-585A-2	Sequence 3, Appl
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15	55.6	2.5	8705	4 US-09-647-344A-14	Sequence 14, Appl
16	55.6	2.5	9600	3 US-08-910-647-1	Sequence 1, Appl
17	55.6	2.5	9600	4 US-09-620-925-1	Sequence 1, Appl
18	55.6	2.5	10596	1 US-07-884-811-15	Sequence 15, Appl
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20	55.6	2.5	10596	1 US-08-087-783A-15	Sequence 15, Appl
21	55.6	2.5	10596	1 US-08-194-088B-15	Sequence 15, Appl
22	55.6	2.5	10596	2 US-08-194-087-15	Sequence 15, Appl
23	55.6	2.5	10596	5 PCT-US93-04648-15	Sequence 15, Appl
24	55.6	2.5	16080	4 US-09-724-566A-48	Sequence 48, Appl
25	48.6	2.2	2299	4 US-09-475-515-81	Sequence 81, Appl
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C 30	47.6	2.2	3525	4 US-09-252-991A-12708	Sequence 12708, A
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C 32	47.6	2.1	2305	4 US-09-475-515-80	Sequence 80, Appl
C 33	47.6	2.1	2306	4 US-09-475-515-82	Sequence 82, Appl
C 34	47.6	2.1	2312	4 US-09-475-515-84	Sequence 84, Appl
C 35	47.6	2.1	4319	4 US-09-475-515-6	Sequence 6, Appl
C 36	46	2.1	330	3 US-09-165-264-13	Sequence 13, Appl
C 37	45.8	2.1	319	3 US-09-165-264-8	Sequence 8, Appl
C 38	45.6	2.1	15231	3 US-09-128-155-16	Sequence 16, Appl
C 39	45.4	2.1	320	3 US-09-165-264-11	Sequence 11, Appl
C 40	45.2	2.0	320	3 US-09-165-264-7	Sequence 7, Appl
C 41	45	2.0	330	3 US-09-165-264-14	Sequence 14, Appl
C 42	44.6	2.0	729	4 US-09-252-991A-11877	Sequence 11877, A
C 43	44.6	2.0	783	4 US-09-252-991A-11569	Sequence 11569, A
C 44	44.4	2.0	1865	4 US-09-370-253-5	Sequence 5, Appl
C 45	44.2	2.0	318	3 US-09-165-264-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-482-180A-1
; Sequence 1, Application US/09482180A
; Patent No. 6361985
; GENERAL INFORMATION:
; APPLICANT: Conkito, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Jaspers, Stephen
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
; FILE REFERENCE: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG, ZNSP6
; CURRENT APPLICATION NUMBER: US/09/482,180A
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/115,721
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(1271)
US-09-482-180A-1
Query Match 8.5%; Score 188.4; DB 4; Length 1420;
Best Local Similarity 51.3%; Pred. No. 1.5e-37;
Matches 531; Conservative 0; Mismatches 481; Indels 24; Gaps 3;
192 CTCCTCTCTTCACTGCTGCTAGTGTACCACTGCAAGTCCAGAGCAGCCACCG 251
231 CTGGTCTGTCAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 290
252 GCGATCCCGAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 311
291 GCCAAGCCCGAGGAGAACCCACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 350
312 CATGCCAACCTTATGTGTACCACTGCGAGCTTGCAGCAGCGAGCGAGCAGCTTAC 371
351 CACAGCGAGGTGCACCAACCAACAGGTGTAGCGCTGCTGCTGCTGCTGCTGCTGCT 410
372 AATCTCTCTGTGACAGACAGCTGCGCAGCTTCCCTGCTGAGAGAGAGTCCCTCT 431
411 CACCGTCTCTTCTGACCTATGCTACGCGCAATTTCTATCTTGTGAGAGCTTCA 470
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Db 471 GGGTGTCCAGAGATACCTTCTTGCTCTGGCCATCAAGTCACAGCTGTGCACGTGAG 530
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Qy 549 CTGGCCCTCTCTCTCTGTTGGGACAGGCTTCAACCCCGACGAGGCGCCGAGGTCAC 608
Db 591 CTGAAGCTGTGTCTCTCTAGGGGGGAGGAGATCCGCTCCCGAGCCCA----- 640
Qy 609 CGGCTGTGAGCTGGAGGACACAGTCAAGAGACATCTGAGTGGGACTTCCAGAC 668
Db 641 --GCTGCTGGCTTANGAGAGTAGAGGAGTGTGATGACATCTCAGTGGGACTTCA 698
Qy 669 TCCCTTCAACCTCAACGCTCAAGAGGCTGTGTTCTTACATGTGGAGAGCAAGTGC 728
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Qy 729 GCGAAGCGGAGCTGTGCTCAACGGGGATGATGACGCTTGTGACACACAGACATG 788
Db 759 CCCCAGGCCCATTTATGCTTAAAGGAGATGACGATGTCTTGTCCAGCTCCCGACAG 818
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Db 939 GGCACCCACTACCCACCTATGCTGTGGGGGAGATGATGATGCCAGGCCACAGTG 998
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Db 999 CGGCGCTGCTCAAGGCTATCATGAAAGTCTGAATCTCTCCATGATGATGCTTGTG 1058
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Db 1059 GGTATGTCTGAGAGGCTGAGGCTGAGCCCTATGACACAGCTGGCTTCAAGATTT 1118
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; OTHER INFORMATION: degenerate sequence
; NAME/KEY: variation
; LOCATION: (1)...(1134)
; OTHER INFORMATION: n is any nucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)...(1134)
; OTHER INFORMATION: n = A,T,C or G
US-09-482-180A-3

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Beet Local Similarity 32.2%; Pred. No. 1.1e-35;
Matches 334; Conservative 154; Mismatches 524; Indels 24; Gaps 3;

Qy 192 CTCCCTCTCTCAAGCTGCTGATGTGACACCCACCTGCAAGTCCAGAGGACGACCG 251
Db 97 YTNGTMSNTYTWMSYTNMGCTNTYTNNGTNTGNTYTNNTYTNMGAARCN 156
Qy 252 GCGATCCCGAGGCGCTGGCTGCGCCACTGACCCAGCCGCGGCGCTGTC 311
Db 157 GCNARCCNGNGNGAYCCNACNGNCAYCARCCNTTYTGGGCGNCNACNCGN 216
Qy 312 CATGCCAACACTCTATAGTACCCAGGACTTGGCAGGAGCCGACGACTTCA 371
Db 217 CAWSNMNTGTCNCCNAAAYCAVANGTMSNMSNMSNTYTNMSTYTNMSTYTNM 276
Qy 372 AACTCTCTCTGTACAGACACTGCGCCACTTCCCTGCTGACAGAGTGCCTCT 431
Db 277 CAYMNTNTYTNMCTATMGNCATYTNMGAAYTNMSTYTNMSTYTNMSTYTNM 336
Qy 432 AAGTGGGCGAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
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Qy 492 CGCCGCGAGCTGCTGCGGCGGACGTCGGGGCCG---CGAGCCGAGTACGGGG 548
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Qy 549 CTGGGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
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Db 685 YTNARNTYTNNGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
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Qy 909 AATGAGCGGTACCCACCTATGTTGGGGTGGTGGCTTCTGCTGCTGCTGCTGCT 968
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Db      865  MGNMNYTNCARGCNATHATGARGAYGNGARYTYTWNMSNATHGAYGNTTGTGN 924
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Db      925  GGNATGTGTCTGAGCTTGAGGACCTGACCTCCACAGCGGACCTCCAGCTCT 984
QY      1089 GGGGTGGGGGCTCCATCGCAACACTGTCTCTCTTTGACCCCTGCTCTACGAGACTG 1148
Db      985  GGNATGTGTCTGAGCTTGAGGACCTGACCTCCACAGCGGACCTCCAGCTCT 1035
QY      1149 CTGCTGTGTGACCGCTCTCTACCTTATGAGATGCTGCTCATGTGGATGCGTGAACGAG 1208
Db      1036 YTYTNGTNCAYMGNATGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1095
QY      1209 CCCAAGCTGACCTGCG 1224
Db      1096 GARGNYTNAARTGYG 1111

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US-09-459-133-3
; Sequence 3, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Konklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1191)
; OTHER INFORMATION: n = A,T,C or G
US-09-459-133-3

Query Match      4.6%; Score 102.2; DB 4; Length 1191;
Best Local Similarity 29.2%; Pred. No. 4.8e-16;
Matches 251; Conservative 122; Mismatches 472; Indels 14; Gaps 4;

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QY      398  CCACTTTCCCTCTCTG---CAGACGTGCCCCCTCTTAAGTGCGGCGACGCTCTCC 453
Db      375  NMSNTTYCCNCACTGTGTGTCNCGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNG 434
QY      454  TGCTGTGTGTGATCAAGTCTCTCCCTAGCAATATGTGCGCGCGAGCTGCTCGCGGCA 513
Db      435  NGAYGTNCCNTATYTYTNTTNGNCGTNAABRMSNGARCCGNGNNGNTTYGCGNABMGNC 494
QY      514  CGTGGGCGCGGACGCGCAAGTACGGGCTTTGCAAGCTGCGCTCTCTCTCTGCTGGGCA 573
Db      495  RG-CNGTNGNGBACNTGCGGWNMSNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 553
QY      574  CAGCTTCAACCCGCGAGAGCGCGCGCAAGTCAACCGGCTGTGTGAGCTGAGGACAGAGA 633
Db      554  GNMNCCNCTNGNNGARCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGN 613
QY      634  CTCACGAGACATCTGTGAGTGGGACTTTCACGACCTCTTCAACCTCAGCTCAAGC 693

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Db      674  AYYTYTNTYNTYNTGCGTGTGNGMNGCAAYGYCCNACNCTNMSNTTYGTYTNGNG 723
QY      754  GGGATGATGACGCTTGTGACACACAGACAACATGTGCTCTACCTGCAGG-----ACC 807
Db      734  CNGARAGAYGAYGCTNTTYGTCAYACNCGNCTNTTYTNGCNCAYYTNGNCGNYTNCNC 793
QY      808  ATGACCTGCGCGCAACTCTTGTGTGTGAGCTGATCCAAAAGTGTGCGCCCATCGGG 867
Db      794  CNGCMNSNCGNMGNSNTTYTAYTNGNGBATNTTYACNARGCNAATCCNYTNGNA 853
QY      868  CTTTGTGAGACAGTACTATGTGCCAGAGGTGTACTCAGATGAGCGGTACCACCT 927
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QY      928  ATTGTGGGGGTGTGTGCTTGTCTGTCCCGCTTCAAGCGCGCTGCGCGCTGCGCTG 987
Db      911  ATGCMNSNCGNNGNCGNTAYGTNATHGCGNMGNTTNGCNCNTGTGYTYTNGMGCNG 970
QY      988  CCCATGTCTTGACATCTTCCCATTTGATGATGCTTCTGTGATGTGTCTGAGCTTG 1047
Db      971  CNGCMNNGNCGNCGNTTTCNTTYTGARGAYGTNTAYACNCGNNTTYTGYATHMGNCY 1030
QY      1048  AGGACTGAAGCTGCTCTCCACAGCGGACATCCGACAGTGTGCGGTGCGGCTTCATCC 1107
Db      1031  TNGNNTYNTGNCNCGARCGNCAACGNGNTTYTNAACNCGNTGCGNCGNAGTNGACNG 1090
QY      1108  AACACCTGCTCTCTTGTGACCCCTGCTTACCGAGACGCTGCTGTGTCACCGCTTC 1167
Db      1091  CNGAYCAITGTGCTNTTYMGAAYTYTNTYNTGNTMGNCNTYNTGNCNCGNCGNWSNA 1150
QY      1168  TACCTTATGAGATGCTGT 1186
Db      1151  THMGNTTNGARCARAYT 1169

RESULT 4
US-09-459-133-1
; Sequence 1, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Konklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)...(1294)
US-09-459-133-1

Query Match      4.3%; Score 94.4; DB 4; Length 1532;
Best Local Similarity 52.2%; Pred. No. 4.7e-14;
Matches 262; Conservative 0; Mismatches 231; Indels 9; Gaps 2;

QY      589  ACGAGGCGCGCAAGTCAACCGGCTGTGTGAGCTGAGGACGACGACGACATCC 648
Db      669  AGCGGGGCGCTGACTGACTAGTGTGAGGAGAGAGCGCTCCTACAGTACGACTCG 728

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QY	649	TGCAGTGGGACCTTCCACGACCTCCTCTTCAACCTACGCTCAAGACAGGTCTCTGTTCTTAC	708
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QY	709	AGTGGCAGGAGACAAAGGTGCGGCAACGCGACGTTGCTGCTCAACGGGAGTATGACGCT	768
Db	789	CCTGGCTGGGCGCGCACTGGCCCCCACTGGAGTTGTCTTGGAGACTCAGACGATGCTCT	848
QY	769	TTGCAACAACAACAACATGTGCTTCTTACCTGACGAC-----CATGACCTGGCGGCC	822
Db	849	TTGTACACACCCCTGCGCTGAGCTCACTGCGGGCCCTGCACTGCTGAGCCCGAA	908
QY	823	ACCTCTTGTGGGGGCACTGATCCAAACGATGGGCGCCCATCCGGGCTTTTGGAGCAAGT	882
Db	909	GCCTTACTGTGGGTAGAGTCTTTACCACGAGCATATGCTCTCGGAAGCAGAGGAGACCTT	968
QY	883	ACTATGTGCCAAGGTGTGACTCAAGATGAGCGGATCCACCTATTTGTGGGGGTGTGTG	942
Db	969	TCTATGTGCCGAGTCTTCTTCCGAAGGTG---GCTACCCAGCTATCAAGCGGGGAGTGTG	1025
QY	943	GCTTTGCTGTCCCGCTTCAACGGCGCGTGCCCTCGCGCGGTGTGCCATGTCTTTGACA	1002
Db	1026	GCTATGCTATTGCGGGGCGCTGGACCTTGGCTGTGCGGGCGGCAAGCCCGTGTGGCAC	1085
QY	1003	TCTTTCCCATGTAGATGTCTTCCGTGGGTATGTGTCTGAGACTTGAAGGAGCTGAAGCCTG	1062
Db	1086	CCTTCCCTTTGAGGAGGCTTACACTGGCCCTTTGATCCAGACCCTGGGCTGTGGTCCCC	1145
QY	1063	CCTCCCAAGGGGCAATCCGAC	1084
Db	1146	AGGCGCCACCGAGGCTTCTCTAC	1167

```

RESULT 5
US-09-459-133-14
/ Sequence 14, Application US/09459133
/ Patent No. 6416988
/ GENERAL INFORMATION:
/ APPLICANT: Conklin, Darrell C.
/ APPLICANT: Yamamoto, Gayle
/ APPLICANT: Jaepers, Stephen R.
/ APPLICANT: Gao, Zeren
/ TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
/ FILE REFERENCE: 98-77
/ CURRENT APPLICATION NUMBER: US/09/459,133
/ CURRENT FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: 60/111,697
/ PRIOR FILING DATE: 1998-12-10
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq For Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 1167
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: degenerate sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(1167)
/ OTHER INFORMATION: n = A,T,C or G
US-09-459-133-14

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Query Match	3.7%;	Score 81.8;	DB 4;	Length 1167;
Best Local Similarity	31.3%;	Pred. No. 6e-11;		
Matches 176; Conservative	75;	Mismatches 302;	Indels 9;	Gaps 2

[illegible]

Db	607	TTNNGGAYTTTYTNAGTGNCTNATYAAYMGNACNTYTNAAAGAYTYTNTYTNACN	666
QY	711	TGGCAGGAGACAAGGTGCGCCACGCCAGCTTCGTCTCAACGGGAGATGATACGTCCTT	770
Db	667	TGGYTNMNCAYCAATGYCCNNGAYGTNAAITYTYGTYTNCAAGTNCARGAYAGCCTTY	726
QY	771	GCACACACAGACAACATGATGTCCTTCACTCGCAGAGACATGACCT-----GGCGGCAC	824
Db	727	GTNCAYATHCNCGNCTYTNNGARARAYTYTNCAACNTYNCNCNAACNTGGCGNMGNSN	786
QY	825	CTCTTCGTGGGACCACTGATCCAAACGTGGGCCCATCCGGGCTTTTGGAGCAAGTAC	884
Db	787	YTNATAYTNNGNNGARATHTTYTAACNCAACNAAACNTYTMGAARCCNGNNGANCNTTY	846
QY	885	TATGTCACAGAGGTGTGACTCAGAAATAGAGGTACCCACCTATTGTGGGGGTGTGGC	944
Db	847	TATGTCNCAARACNTTYYTGARGNGA---YTAACNCGNTATGCMWSNNGNNGN	903
QY	945	TTCTTGCTGTCCCGCTTACGAGCGCGCTGACCTCGCGCGGTGTGCCATGTCTTGGACATC	1004
Db	904	TAYGTNATHMNSNGMNGYTNCGNCNTGTATYTNCAAGCNGCNGMNGTNGCNCN	963
QY	1005	TTCCCACTGATGATGTCTTCTCGGTATGTGTCTGAGACTTGAAGGACTGAAGCTGCC	1066
Db	964	TTTCNTTYGAYGAYGTATACNCGANTTYTGTYTMNGCNYTNNGYTNCGNCNNGN	1023
QY	1065	TCCCAACAGCGCATCCGCACGTCGTGGCGGTGCGGCTCATGCACACACTGTCTCTCTT	1122
Db	1024	GCNCAYCNGNGNTTYTNACNGCNTGGCNGCNGABMGNACMGAGATCCTGTGYCNGNTN	1083
QY	1125	GACCCCTGCTTCAACCGAGACC	1146
Db	1084	MNGANTYTNNTYTNCAATC	1105

```

RESULT 6
US-09-459-133-12
; Sequence 12, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaepfers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)...(1273)
US-09-459-133-12

```

Query Match	3.5%	Score 77.8;	DB 4;	Length 1446;
Best Local Similarity	50.7%;	Pred. No. 6.5e-10;		
Matches 243; Conservative	0;	Mismatches 227;	Indels 9;	Gaps 2

Accession	Sequence	Position
Oy	CTGCTGGAGCTGGAGGGACAGACTCACGGAAACATCCGACAGTGGGACTTCCACAGCATCC	671
Oy	612	
Db	CTGCTGACGTGGGAAAGCCGGCCGTATGATGATCACTGCTCTGGGAATTTCTCGATGATTT	733
Db	674	
Oy	672 TTCTTCAACTCAGCGCTCAGCAGAGCTCTGTCTTCAAGTGGCAGGACACAAGGTGCGCC	731
Oy	734 CCTTACACACCGGACACTTCAAGGACCTGTGCTGTGACCTTGGCTGAGCCACATCGGCC	793
Db		

Qy 732 AACGCGCTTGTGCTCAACGGGATGATGACCTTTTGACACAGACAACATGATC 791
Db 794 GATGTCAATTTTGTCTGACAGTTTCAGATGATGATGATGATGATGATGATGATG 853
Qy 792 TTCTACCTGACAGACATGACCC-----TGGCCGCACTCTTTGTGGGCAACATGATC 845
Db 854 GACACCTGACAGCTGACACCCACCTGGGCGCCGACGCTTACCTGGGATGATCTTC 913
Qy 846 CAAACGTGGGCCCCCATCCGGGCTTTTGGAGCAAGATGATGATGATGATGATGATG 905
Db 914 ACCGAGCCCAACCGCTCTCCCAAGCCCGAGAGAACCTTTATGATGATGATGATGATG 973
Qy 906 CAGATGAGCGGATACCACTATTTGATGATGATGATGATGATGATGATGATGATGATG 965
Db 974 ---GAGGGGACATCTACAGCTTATGATGATGATGATGATGATGATGATGATGATG 1030
Qy 966 GCGGCTGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1025
Db 1031 GCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
Qy 1026 CTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1084
Db 1091 ACTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149

RESULT 7
US-09-055-097-2
Sequence 2, Application US/09055097
Patent No. 5955282
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,097
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0490 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: DIODNOT02
CLONE: 1705085
US-09-055-097-2

Query Match 3.4%; Score 74.2; DB 2; Length 1434;
Best Local Similarity 52.0%; Pred. No. 5.2e-09;
Matches 191; Conservative 0; Mismatches 173; Indels 3; Gaps 1;

Qy 437 CGGCGACCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
Db 240 CGGGGCGCCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 299
Qy 497 CGAGCTGCTGCGGCGACGCTGCGGCGCGAGCCCAAGTACGGGGTTTGCAGCTGCGCCT 556
Db 300 AAACGCCATTGCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
Qy 557 CCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
Db 360 GCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 419
Qy 614 GCTGAGCTGAGAGCAGACTCAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
Db 420 CTGGGCTGAGATCAGAGAGCCAGGGGATATCTTGGAGAGGCGGCTTCCAGGACTCTTA 479
Qy 674 CTTCACCTCAGCTCAGAGAGTCTGTTCTTACAGTGGCAGAGACAAAGTGGCGCAA 733
Db 480 CCGCAACTCACCCTAAAGACCTCAGCGGCTGAACTGGGCTGAGAAACACTGCCCAT 539
Qy 734 CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
Db 540 GCGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
Qy 794 CTACCTG 800
Db 600 AGAGCTG 606

RESULT 8
US-09-373-902-2
Sequence 2, Application US/09373902
Patent No. 6649737
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/373,902
FILING DATE: 12-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/055,097
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0490 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:

```

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZpL-F15
US-08-232-463-14

Query Match      2.7%; Score 59.8; DB 1; Length 7218;
Best local similarity 5.4%; Pred. NO. 3.8e-05;
Matches 22; Conservative 225; Mismatches 162; Indels 0; Gaps 0;

QY      TCATTCCTAGCAGCGGCGCCAGACCCAGAGACCGGCCAGAGAGCTCTCTCAGCGGAGCC 109
DB      TTAATCCGACTTGCTGCAGGTGAGGGAGCTGCAATATTTTATTTTTTTTTTTTTT 1086
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      50 TCATTCCTAGCAGCGGCGCCAGACCCAGAGACCGGCCAGAGAGCTCTCTCAGCGGAGCC 109
DB      TTAATCCGACTTGCTGCAGGTGAGGGAGCTGCAATATTTTATTTTTTTTTTTTTT 1086
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      110 CAGACCCTGGTGCGAGATGAATATCTCCGACACCGCGGCCAATGCCACTTCAT 169
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      1087 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1146
DB      YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1146
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      170 TCTGGCATCGGCGCTTACCTCTCTCTCTCAGTGTCTAGTACACCACTGCTG 229
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      1147 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1206
DB      YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1206
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QY      230 CAAGTCCAGAGCAGCACCGGAGATCCCGAGGCGCTGCGCTGACCTCAACCCAG 289
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      1207 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1266
DB      YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1266
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      290 CGCCGAGCCCCGCGCCGCTGATGACCAACTTAATGTACCAACCGGACTTGGC 349
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      1267 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1322
DB      YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1322
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QY      350 CACGACCGCGAGCAGCTTCAAACTTCTCTGTAAGACAGACCTGCGCGCACTTCCCT 409
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      1327 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1387
DB      YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1387
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QY      410 GCAGCAGCAGTGCCTCTAAGTGCAGCGAGCGAGCTTCTGCTG 458
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      1387 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYG 1435
DB      YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYG 1435

RESULT 10
US-09-249-585A-2/c
Sequence 2, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Hotlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISEMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1926)
OTHER INFORMATION: coding strand of EBNA-1 DNA

```


US-09-249-585A-2

Query Match 2.5%; Score 55.6; DB 4; Length 1926;
Best Local Similarity 48.6%; Pred. No. 0.00026;
Matches 210; Conservative 0; Mismatches 219; Indels 3; Gaps 2;

QY 138 CTCGCGACCGGCGGCGCAATGCACTTCTGAGCATGCGCGCTTTCACCTCTC 197
DB 724 CTCCTGCGCCCTCTGCTGCTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTG 665
QY 198 CTCCTGAGTGTGCTAGTGTACCACTGAGTGTGAGAGAGAGAGAGAGAGAG 257
DB 664 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
QY 258 CCGGAGGCGCTG-GCGTGGCGCACTGCAAGCGCGCGCGCGCGCGCGCGCGAG 316
DB 604 CCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545
QY 317 CAACACTCTATAGTACCACTGCGGAGCTTTCGCGAC--GGAGCGGAGAGAGAG 374
DB 544 CTGCGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
QY 375 TTCCTCTGTAGACAGACATGCGCGCACTTTCCTGCTGAGAGAGAGAGAGAG 434
DB 484 CTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
QY 435 TGGGCGAGCGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
DB 424 CCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 365
QY 495 CCGGAGCTGCTGCGGCGAGAGTGGGCGCGGAGAGAGAGAGAGAGAGAGAGAG 554
DB 364 CTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305
QY 555 CTCCTCTGCTG 566
DB 304 CTCCTGCTGCTG 293

RESULT 11

US-09-410-399-3/c
; Sequence 3, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein-Barr virus
US-09-410-399-3

Query Match 2.5%; Score 55.6; DB 4; Length 1926;
Best Local Similarity 48.6%; Pred. No. 0.00026;
Matches 210; Conservative 0; Mismatches 219; Indels 3; Gaps 2;

QY 138 CTCGCGACCGGCGGCGCAATGCACTTCTGAGCATGCGCGCTTTCACCTCTC 197
DB 724 CTCCTGCGCCCTCTGCTGCTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTG 665
QY 198 CTCCTGAGTGTGCTAGTGTACCACTGAGTGTGAGAGAGAGAGAGAGAGAG 257
DB 664 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
QY 258 CCGGAGGCGCTG-GCGTGGCGCACTGCAAGCGCGCGCGCGCGCGCGCGAG 316
DB 604 CCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545

DB 604 CCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545

QY 317 CAACACTCTATAGTACCACTGCGGAGCTTTCGCGAC--GGAGCGGAGAGAGAG 374
DB 544 CTGCGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485

QY 375 TTCCTCTGTAGACAGACATGCGCGCACTTTCCTGCTGAGAGAGAGAGAGAGAG 434
DB 484 CTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
QY 435 TGGGCGAGCGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
DB 495 CCGGAGCTGCTGCGGCGAGAGTGGGCGCGGAGAGAGAGAGAGAGAGAGAGAG 554
QY 364 CTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305
DB 304 CTCCTGCTGCTG 293

RESULT 12

US-09-050-863-2/c
; Sequence 2, Application US/09050863
; Patent No. 6114111
; GENERAL INFORMATION:
; APPLICANT: Lao, Ying
; APPLICANT: Hiang, Betty
; APPLICANT: Payan, Don
; TITLE OF INVENTION: Mammalian Protein Interaction Cloning
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/050,863
; FILING DATE: 30-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 949-8711
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-09-050-863-2

Query Match 2.5%; Score 55.6; DB 3; Length 2580;
Best Local Similarity 48.6%; Pred. No. 0.00029;
Matches 210; Conservative 0; Mismatches 219; Indels 3; Gaps 2;

QY 138 CTCGCGACCGGCGGCGCAATGCACTTCTGAGCATGCGCGCTTTCACCTCTC 197
DB 1107 CTCCTGCGCCCTCTGCTGCTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTG 1048

[illegible]

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Best Local Similarity	48.6%;	Pred. No. 0.00046;		
Matches 210;	Conservative 0;	Mismatches 219;	Indels 3;	Gaps 2;

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Db	7563	CTCCGCCCCCTCAGCTCTGTGCCCTCTGTGCTCCGAGCCCTCTCGGCCCTCTTGCCCCCTC	7622
Qy	198	CTCTTTCACTCTGCTAGTGTACAACCAACTGTGAAGTTCAGAGAAGCACTCACGGGCATC	257
Db	7623	CTCTGCTCTGCCCCCTCTCTGCTCTGTGCCCTCTCTGCCCCCTCTGCCCCCTCTCTGCTCTG	7682
Qy	258	CCCGAGGCGCTG-GCTGGGCCCATCTCAACCAACCGGCGAGCCCCGGGCCGTCAGTC	316
Db	7683	CCCCTCTCTGCTCTGTGCCCCCTCTGCCCCCTCTGAGCCCCCTCTCTGCTCTGTGCCCCCTC	7742
Qy	317	CAAACCTCTAATGCTCACCAACCCGGACTTTCGCAAC-GCAGCGGACAGATTTCAAGAC	374
Db	7743	CTGCCCCCTCTCTGCTCTGTGCTGCTCTCTCTCTGCTCTGAGCCCCCTCTGAGCCCCCTCTGAGC	7802
Qy	375	TTCCTCCCTGTACAGACATGCGCGGCACTTTCCTCTGTCAGAGACGTGCCCTCTTAAG	434
Db	7803	CTCTCTCTGCTCTGCCCCCTCTCTGCCCCCTCTCTCTGCTCTGAGCCCCCTCTCTGCTCTG	7862

QY	435	TGCGGAGAGCGGGCTTCCTGCTGCTGATGATCAAGTCCTCCCTAGCACTAATGTGGC	494
Db	7863	CCCTCTGCCCCCTCTGCCCCCTCTCTGCTCTTCTGCCCCCTCTCTGCTCTGCCCCCTC	7922
QY	495	CGCAGAGCTGCTGCGGCGCAGCTGGGGCGCGCAGCGCAAGTACGGGGTTTGACCTGGC	554
Db	7923	CTGGCCCCCTCTGCCCCCTCTGCCCCCTCTCTGCTCTCTGCCCCCTCTCTGCTCTGCCC	7982
QY	555	CTCCTCTTCTCG	566
Db	7983	CTCCCTGCTCTCG	7994

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Search completed: June 14, 2004, 10:09:03
Job time : 164 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 14, 2004, 10:23:39 ; Search time 1789 Seconds
(without alignments)
5625.902 Million cell updates/sec

Title: US-10-019-735-6

Perfect score: 2205

Sequence: 1 ggcacaggaaccgcgaagcg.....aaaattctgtaagacttg 2205

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2998549 seqs, 2282253817 residues

Total number of hits satisfying chosen parameters: 5997098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2119.8	96.1	2210	13	US-10-206-915-287
2	2119.8	96.1	2210	13	US-10-199-670-287
3	2119.8	96.1	2210	13	US-10-201-858-287
4	2119.8	96.1	2210	13	US-10-205-890-287
5	2119.8	96.1	2210	13	US-10-208-024-287
6	2119.8	96.1	2210	13	US-10-201-853-287
7	2119.8	96.1	2210	13	US-10-174-581-287
8	2119.8	96.1	2210	13	US-10-176-483-287
9	2119.8	96.1	2210	13	US-10-176-749-287
10	2119.8	96.1	2210	13	US-10-176-914-287
11	2119.8	96.1	2210	13	US-10-176-915-287
12	2119.8	96.1	2210	13	US-10-176-484-287
13	2119.8	96.1	2210	13	US-10-180-550-287
14	2119.8	96.1	2210	13	US-10-183-014-287

15	2119.8	96.1	2210	13	US-10-187-738-287	Sequence 287, App
16	2119.8	96.1	2210	13	US-10-187-740-287	Sequence 287, App
17	2119.8	96.1	2210	13	US-10-187-883-287	Sequence 287, App
18	2119.8	96.1	2210	13	US-10-194-363-287	Sequence 287, App
19	2119.8	96.1	2210	13	US-10-194-460-287	Sequence 287, App
20	2119.8	96.1	2210	13	US-10-194-463-287	Sequence 287, App
21	2119.8	96.1	2210	13	US-10-194-484-287	Sequence 287, App
22	2119.8	96.1	2210	13	US-10-195-884-287	Sequence 287, App
23	2119.8	96.1	2210	13	US-10-195-896-287	Sequence 287, App
24	2119.8	96.1	2210	13	US-10-196-744-287	Sequence 287, App
25	2119.8	96.1	2210	13	US-10-196-755-287	Sequence 287, App
26	2119.8	96.1	2210	13	US-10-196-757-287	Sequence 287, App
27	2119.8	96.1	2210	13	US-10-197-704-287	Sequence 287, App
28	2119.8	96.1	2210	13	US-10-197-710-287	Sequence 287, App
29	2119.8	96.1	2210	13	US-10-198-758-287	Sequence 287, App
30	2119.8	96.1	2210	13	US-10-198-766-287	Sequence 287, App
31	2119.8	96.1	2210	13	US-10-199-304-287	Sequence 287, App
32	2119.8	96.1	2210	13	US-10-199-309-287	Sequence 287, App
33	2119.8	96.1	2210	13	US-10-199-313-287	Sequence 287, App
34	2119.8	96.1	2210	13	US-10-199-456-287	Sequence 287, App
35	2119.8	96.1	2210	13	US-10-201-329-287	Sequence 287, App
36	2119.8	96.1	2210	13	US-10-202-412-287	Sequence 287, App
37	2119.8	96.1	2210	13	US-10-206-919-287	Sequence 287, App
38	2119.8	96.1	2210	13	US-10-206-922-287	Sequence 287, App
39	2119.8	96.1	2210	13	US-10-206-924-287	Sequence 287, App
40	2119.8	96.1	2210	13	US-10-206-928-287	Sequence 287, App
41	2119.8	96.1	2210	13	US-10-207-914-287	Sequence 287, App
42	2119.8	96.1	2210	13	US-10-207-921-287	Sequence 287, App
43	2119.8	96.1	2210	13	US-10-207-922-287	Sequence 287, App
44	2119.8	96.1	2210	13	US-10-208-027-287	Sequence 287, App
45	2119.8	96.1	2210	13	US-10-174-570-287	Sequence 287, App

ALIGNMENTS

RESULT 1
US-10-206-915-287
; Sequence 287, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206, 915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28

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/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 287
/ LENGTH: 2210
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-206-915-287

Query Match      96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
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QY 78 GGAGCGCCCGCAGAGGCTCTCAAGGCGGACCCAGACCTGAGTGGCCAGATGAAATAT 137
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QY 138 CTCGGGACCGGCGGCGCCCAATGCACTCATTTGAGCCATGCGGCTTTCACTCTCTC 197
Db 112 CTCGGGACCGGCGGCGCCCAATGCACTCATTTGAGCCATGCGGCTTTCACTCTCTC 171
QY 198 CTCCTTACGTCTGTAATGTACCAACCACTGTAAGTTCAGAGAGAGCAACGGGATC 257
Db 172 CTCCTTACGTCTGTAATGTACCAACCACTGTAAGTTCAGAGAGAGCAACGGGATC 231
QY 258 CCGGAGGCGCTGAGCTGAGCCCACTCCAGCCACCGGCGGCGGCGGCGGCGGATC 317
Db 232 CCGGAGGCGCTGAGCTGAGCCCACTCCAGCCACCGGCGGCGGCGGCGGCGGATC 291
QY 318 AACACCTATATGTATCAACCCAGACTTTCGCAAGCGGCGGCGGCGGCGGATC 377
Db 292 AACACCTATATGTATCAACCCAGACTTTCGCAAGCGGCGGCGGCGGCGGATC 351
QY 378 CTCCTTACGACACACGCGGCGCACTTCCCTGCGAGAGAGTGGCGGCGGCGGATC 437
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QY 438 GCGCAGCGGCTCTTCTGCTGCTGTGTATCAAGTCTCCCTTACCAATATGTGCGCGC 497
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QY 498 GAGCTGCTGCGGCGCACTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGATC 557
Db 472 GAGCTGCTGCGGCGCACTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGATC 531
QY 558 CTCCTTCTGAGGCGACAGGCTCCACCCGCGAGAGGCGGCGGCGGCGGCGGATC 617
Db 532 CTCCTTCTGAGGCGACAGGCTCCACCCGCGAGAGGCGGCGGCGGCGGCGGATC 591
QY 618 GAGCTGAGGCGACAGCTCAAGAGATCTGAGTGGGACTTTCAGAGCTCTCTTCTTC 677
Db 592 GAGCTGAGGCGACAGCTCAAGAGATCTGAGTGGGACTTTCAGAGCTCTCTTCTTC 651
QY 678 AACCTCAAGCTCAAGAGAGTCTGTTTCAAGTGGAGAGAGCAAGTGGCGGCGGCGG 737
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QY 738 AGCTTCTGCTCAAGGCGGATGATGAGCTTTTGACACACAGACCAATGCTTCTTAC 797
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Db 892 TACCACCTATATGTGAGGAGTGTGCTTCTGCTGTCCGCTTACGCGCGCTGCGCTG 951
QY 978 GCGGCTGCTGCGCAATGCTTTGAGACATCTTCCCATATGATGCTTCTGAGGATGCT 1037
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QY 1458 AGGAACTCCAGAAATATGATCTTCTTTTGTGCTGCTAATGCGAGAGGCTGTC 1517
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QY 1878 AGTTGAGAGCTCAGAGTTCTGAGGAGTCTGATTAAGAGCCCGCATCCCTGTGTC 1937
Db 1852 AGTTGAGAGCTCAGAGTTCTGAGGAGTCTGATTAAGAGCCCGCATCCCTGTGTC 1911
QY 1938 AAGAAATCAAGAGAGAGCACTGGGCGCTGAATGATTTTAAATGGGCGCAAGCAAG 1997
Db 1912 AAGAAATCAAGAGAGAGCACTGGGCGCTGAATGATTTTAAATGGGCGCAAGCAAG 1971
QY 1998 CATATCCCTCACTATGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2057
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Db	1972	CATPAGCCCTCAGTACTGCTGGAGAAGGGAAGAAATTACAGTCTCTCGACGAGCCTCCTCA	2038
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Qy	2178	GCGAATATAAATTTTGTGAGA	2200
Db	2152	GCGAATATAAATTTTGTGAGA	2174
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; Sequence 287, Application US/10199670			
; Publication No. US20040033560A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jien			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Aueelin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3430R1C401			
; CURRENT APPLICATION NUMBER: US/10/199, 670			
; CURRENT FILING DATE: 2002-07-19			
; PRIOR APPLICATION NUMBER: 10/052586			
; PRIOR FILING DATE: 2002-01-15			
; PRIOR APPLICATION NUMBER: 60/059263			
; PRIOR FILING DATE: 1997-09-18			
; PRIOR APPLICATION NUMBER: 60/059266			
; PRIOR FILING DATE: 1997-09-18			
; PRIOR APPLICATION NUMBER: 60/062250			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/063120			
; PRIOR FILING DATE: 1997-10-24			
; PRIOR APPLICATION NUMBER: 60/063121			
; PRIOR FILING DATE: 1997-10-24			
; PRIOR APPLICATION NUMBER: 60/063486			
; PRIOR FILING DATE: 1997-10-21			
; PRIOR APPLICATION NUMBER: 60/063540			
; PRIOR FILING DATE: 1997-10-28			
; PRIOR APPLICATION NUMBER: 60/063541			
; PRIOR FILING DATE: 1997-10-28			
; PRIOR APPLICATION NUMBER: 60/063544			
; PRIOR FILING DATE: 1997-10-28			
; Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO 287			
; LENGTH: 2210			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-199-670-287			
 Query Match 96.1%; Score 2119.8; DB 13; Length 2210;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	78	GGAGCCGCCACGAGGAGGCTCTCAGGCCGACCCGACGACCTGCTGGCCAGATGAAGTAT	137
Db	52	GGAGCCGCCACGAGGAGGCTCTCAGGCCGACCCGACGACCTGCTGGCCAGATGAAGTAT	111
Qy	138	CTCCGGCACCGGCGGCCAACATCCACCTTCATTTGGCCATGCGCGCTTTACCTCTTC	197

Db	112	CTCCGGACACGGCGGGCCCAATGCAACCCCTCATTTCTGGCCATCGGGCTTTACACCTCTCTC	171
Qy	198	CTCTTCAGTCTGCTAGTGTGACACACCACTTGCAAGTTCAGAGACAGCAACGGCGATC	257
Db	112	CTCTTCAGTCTGCTAGTGTGACACACCACTTGCAAGTTCAGAGACAGCAACGGCGATC	231
Qy	258	CCCGAGGCCCTGGCCCTGGCCCACTTCACCCACCCGCCCAAGCCCGGCCCTGGTCCATGCC	317
Db	232	CCCGAGGCCCTGGCCCTGGCCCACTTCACCCACCCGCCCAAGCCCGGCCCTGGTCCATGCC	291
Qy	318	AACACCTCTAATGATACCCACCCCGGACCTTCGCAAGCGAGCCGACACAGTTTCAGAACTTC	377
Db	292	AACACCTCTAATGATACCCACCCCGGACCTTCGCAAGCGAGCCGACACAGTTTCAGAACTTC	351
Qy	378	CTCTCTGTACAGACATCTGCGGCACTTTTCCCTCGCTGCGAGAGAGTGTCCCTCTTAAGTGC	437
Db	352	CTCTCTGTACAGACATCTGCGGCACTTTTCCCTCGCTGCGAGAGAGTGTCCCTCTTAAGTGC	411
Qy	438	GCGAGACCGGATCTTCTGCTGCTGATGATCAAGTCTCTCCCTTAGCAATATGTGCGCGC	497
Db	412	GCGAGACCGGATCTTCTGCTGCTGATGATCAAGTCTCTCCCTTAGCAATATGTGCGCGC	471
Qy	498	GAGCTGTGCGGCGGACGTGGGGCCGCGAGGCGCAAGGTATCGGGTTTGTGACGTGGCGCTC	557
Db	472	GAGCTGTGCGGCGGACGTGGGGCCGCGAGGCGCAAGGTATCGGGTTTGTGACGTGGCGCTC	531
Qy	558	CTCTTCTGTGGGGGACAGACCTCCAAACCGGACGAGGGCCGCAAGGTCAACGGGCTGGCT	617
Db	532	CTCTTCTGTGGGGGACAGACCTCCAAACCGGACGAGGGCCGCAAGGTCAACGGGCTGGCT	591
Qy	618	GAGCTGAGGACACAGACTCAGGAGACATCTCTGAGTGGGACTTTCACAGACTCTTCTTTC	677
Db	592	GAGCTGAGGACACAGACTCAGGAGACATCTCTGAGTGGGACTTTCACAGACTCTTCTTTC	651
Qy	678	AACTCTAAGCTTCAGAGAGTCTCTGTTCTTACATGTGCGAGAGACAAAGTGGGCCAACGCC	737
Db	652	AACTCTAAGCTTCAGAGAGTCTCTGTTCTTACATGTGCGAGAGACAAAGTGGGCCAACGCC	711
Qy	728	AGCTTCGATGCCAACGGGAGATGATGAGTCTTTTGACACACAGACCAATGGTCTTCTTAC	797
Db	712	AGCTTCGATGCCAACGGGAGATGATGAGTCTTTTGACACACAGACCAATGGTCTTCTTAC	771
Qy	798	CTGCAGAGCAATGACCCCTGGCCGCCACTCTTCTGTGGGGCAACTGATCCAAAACGTGGGAC	857
Db	772	CTGCAGAGCAATGACCCCTGGCCGCCACTCTTCTGTGGGGCAACTGATCCAAAACGTGGGAC	831
Qy	858	CCCATCCGGGCTTTTGTGAGGACAGTACTATGTGCCAGAGGTGTGACTCAGAAATGACGGG	917
Db	832	CCCATCCGGGCTTTTGTGAGGACAGTACTATGTGCCAGAGGTGTGACTCAGAAATGACGGG	891
Qy	918	TACCAACCCCTAATGTGGGGGGGTGGTCTTGTGGTCCCGCTTCAACGGCCGGCTGGCCCTG	977
Db	892	TACCAACCCCTAATGTGGGGGGGTGGTCTTGTGGTCCCGCTTCAACGGCCGGCTGGCCCTG	951
Qy	978	GCGGTGTGCGCAATGTCTTGGACATCTTCCCAATGATGATGTCTTCTGGGATATGTGT	1037
Db	952	GCGGTGTGCGCAATGTCTTGGACATCTTCCCAATGATGATGTCTTCTGGGATATGTGT	1011
Qy	1038	CTGAGCTTGAAGGACCTGAAGCTTGGCTCCCAACGGGCAATCCGACGATCTGGCGTGGCGG	1097
Db	1012	CTGAGCTTGAAGGACCTGAAGCTTGGCTCCCAACGGGCAATCCGACGATCTGGCGTGGCGG	1071
Qy	1098	GCTCCATGTGGCAACCTGTCTCTCTTTGACCCCGCTTCTTACGAGACCTGTCTGTGTG	1157
Db	1072	GCTCCATGTGGCAACCTGTCTCTCTTTGACCCCGCTTCTTACGAGACCTGTCTGTGTG	1131
Qy	1158	CACCGCTTCTTACCTTATGAGATCTGTCTGATGTGGGATGGGCTGAACCAAGCCCAACTC	1217
Db	1132	CACCGCTTCTTACCTTATGAGATCTGTCTGATGTGGGATGGGCTGAACCAAGCCCAACTC	1191
Qy	1218	ACCTGGGCAATCAGACACAGATCTTACTGATCAGATCAGGGTCCCAAGCTTGTGGCT	1277

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Db      1192 ACCTGGGCAATCAGACACAGATCTAAGTCAGATCATGGGATGCCCAAGCTTGAGCT 1251
QY      1278 CCTGTTTCCAGAGAAAGGGCCGACACCTTCTCTCCAGAAAGCTGAGACCTTTGTGTCTG 1337
Db      1252 CCTGTTTCCATAGGAAGGGCCGACACCTTCTCTCCAGAAAGCTGAGACCTTTGTGTCTG 1311
QY      1338 AACATAGGAGGAGCCAGGAAAGGTTTGAAGTTTGAATGATGAAATTTCTGGCTGGCGAA 1397
Db      1312 AACATAGGAGGAGTCCAGGAAAGGTTTGAAGTTTGAATGATGAAATTTCTGGCTGGCGAA 1371
QY      1398 CTCCTACACATCTTCAAAACCACCTGGTACTGTTCCAGACATCTTCCCTGAGTGGCTG 1457
Db      1372 CTCCTACACATCTTCAAAACCACCTGGTACTGTTCCAGACATCTTCCCTGAGTGGCTG 1431
QY      1458 AGGAATCTCAGAAATATGATCTTTTGTGGTGTCTAATGGCAGAAAGTCCGTGTC 1517
Db      1432 AGGAATCTCAGAAATATGATCTTTTGTGGTGTCTAATGGCAGAAAGTCCGTGTC 1491
QY      1518 TAGAGTTCCAGCTGGAGTGCATCCGTCGTTTGATGCAAAAGTCTTACTTCCCTGCTCT 1577
Db      1492 TAGAGTTCCAGCTGGAGTGCATCCGTCGTTTGATGCAAAAGTCTTACTTCCCTGCTCT 1551
QY      1578 CACCTACTCAGACAGCGGATGCTAAGCAGTGCACCTGAGTGTATTAATGGCAGATTAAC 1637
Db      1552 CACCTACTCAGACAGCGGATGCTAAGCAGTGCACCTGAGTGTATTAATGGCAGATTAAC 1611
QY      1638 TCCGTCGTGAGTTCCAGGCGCAGCCAGAACTCTGTGTCTCAATGAGCTGACGTGAGA 1697
Db      1612 TCCGTCGTGAGTTCCAGGCGCAGCCAGAACTCTGTGTCTCAATGAGCTGACGTGAGA 1671
QY      1698 ATATCTTTTCCAGCCAGAGAGAGGGGTCCTGATCTTAACCTTTCTGGGCTCAGACAA 1757
Db      1672 ATATCTTTTCCAGCCAGAGAGAGGGGTCCTGATCTTAACCTTTCTGGGCTCAGACAA 1731
QY      1758 CTCAGAGGTTGGGGGATACAGAGAGTGTGGAATAGAACCGGCCCTCTCTTAATTG 1817
Db      1732 CTCAGAGGTTGGGGGATACAGAGAGTGTGGAATAGAACCGGCCCTCTCTTAATTG 1791
QY      1818 TGGGATCAAAATGCTGTAATGTGTGAGAGTGTGGCAGAGAGGAGGCAAGTGTCTTGA 1877
Db      1792 TGGGATCAAAATGCTGTAATGTGTGAGAGTGTGGCAGAGAGGAGGCAAGTGTCTTGA 1851
QY      1878 AGTTGAGAGGCTCAGAGTTTCTGGGCTCTCATTTAGAGCCGCCATCCCTGTGTTCC 1937
Db      1852 AGTTGAGAGGCTCAGAGTTTCTGGGCTCTCATTTAGAGCCGCCATCCCTGTGTTCC 1911
QY      1938 AAGAAATTCAGAGAACAGCACTGGGGCTGGAATGATCTTTAATGGGCCCAAGGCCAAC 1997
Db      1912 AAGAAATTCAGAGAACAGCACTGGGGCTGGAATGATCTTTAATGGGCCCAAGGCCAAC 1971
QY      1998 CATATGCCCTCACTACTGCTGAGAGAGGAGATTCAGGTCTTCCAGCAGCTCTCCCTCA 2057
Db      1972 CATATGCCCTCACTACTGCTGAGAGAGGAGATTCAGGTCTTCCAGCAGCTCTCCCTCA 2031
QY      2058 CCCAGATGTTTACAGATTAACGGGGGAGACCGGGGTAGCCAGTGAACCCCTGAGGCC 2117
Db      2032 CCCAGATGTTTACAGATTAACGGGGGAGACCGGGGTAGCCAGTGAACCCCTGAGGCC 2091
QY      2118 AGCTTCAGGCTCAGTGTCTGACAGTCAAGCTTCAAGGCAATTTGTATGGGAGGCTTG 2177
Db      2092 AGCTTCAGGCTCAGTGTCTGACAGTCAAGCTTCAAGGCAATTTGTATGGGAGGCTTG 2151
QY      2178 GGGAAATATAAATTTTGTGAGA 2200
Db      2152 GGGAAATATAAATTTTGTGAGA 2174
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RESULT 3
US-10-201-858-287
; Sequence 287, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C464
CURRENT APPLICATION NUMBER: US/10/201,858
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 287
LENGTH: 2210
TYPE: DNA
ORGANISM: Homo Sapien
US-10-201-858-287

Query Match      96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      78  GGAGCCGCCAGAGAGGCTCTCAGAGCCGACCCCAAGCCTTGCTGCGCAGATGAATAT 137
Db      52  GGAGCCGCCAGAGAGGCTCTCAGAGCCGACCCCAAGCCTTGCTGCGCAGATGAATAT 111
QY      138  CTCGGGACACCGGCGCCCAATGCAACCTCATTTGCGCATGAGGCGTTTCAACCTCCCTC 197
Db      112  CTCGGGACACCGGCGCCCAATGCAACCTCATTTGCGCATGAGGCGTTTCAACCTCCCTC 171
QY      198  CTCCTCAGCTGCTAGTGTGACCAACCACTGCAAGTCCAGAGAGGCAACCGGAGATC 257
Db      172  CTCCTCAGCTGCTAGTGTGACCAACCACTGCAAGTCCAGAGAGGCAACCGGAGATC 231
QY      258  CCCGAGGCGCTTGCTGCTGACCTGACCACTGACCACTGCGCCAGCGCCGCGCCGTCATGCC 317
Db      232  CCCGAGGCGCTTGCTGCTGACCTGACCACTGACCACTGCGCCAGCGCCGCGCCGTCATGCC 291
QY      318  AACACCTCTATAGTCAACCAACCGGACTTGGCAGCGAGCCGCAAGCACTTGAATCTTC 377
Db      292  AACACCTCTATAGTCAACCAACCGGACTTGGCAGCGAGCCGCAAGCACTTGAATCTTC 351
QY      378  CTCCTGTACAGACACGCGCGCACTTCCCTGCTGACAGAGTGGCCCTCTAAGTGC 437
Db      352  CTCCTGTACAGACACGCGCGCACTTCCCTGCTGACAGAGTGGCCCTCTAAGTGC 411
QY      438  GCGCAGCGGCTTCTCTGCTGCTGATCAAGTCTCCCTAAGCACTATGTGCGCGC 497
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Db 412 GCGCAGCCGGTCTTCCGTGCTGTGTATCAAGTCTCCCTAGCAACTATATGTGCGCGC 471
Qy 498 GAGCTCTGTGGGCGACGTGGGGCCGCGAGCGCAAGTACGGGGTTTGGACGTGCGCCTC 557
Db 472 GAGCTCTGTGGGCGACGTGGGGCCGCGAGCGCAAGTACGGGGTTTGGACGTGCGCCTC 531
Qy 558 CTCTTCTGTGGGCGACAGCTTCAACCCGCGACGAGGCCCGGCAAGGTCAACCGGCTGCTG 617
Db 532 CTCTTCTGTGGGCGACAGCTTCAACCCGCGACGAGGCCCGGCAAGGTCAACCGGCTGCTG 591
Qy 618 GAGCTGAGGCGACAGCTCAACGAGACATCTGCACTGGGACCTTCCACGACTCTCTTCTTC 677
Db 592 GAGCTGAGGCGACAGCTCAACGAGACATCTGCACTGGGACCTTCCACGACTCTCTTCTTC 651
Qy 678 AACCTCAAGCTCAAGAGGTCTCTTCTTACAGTGGGAGAGACAAAGTGGCGCAAGCGC 737
Db 652 AACCTCAAGCTCAAGAGGTCTCTTCTTACAGTGGGAGAGACAAAGTGGCGCAAGCGC 711
Qy 738 AGCTTGTGTCAACGGGGATGATGACGTCTTGGACACAGACAAACATGTCTTCTAC 797
Db 712 AGCTTGTGTCAACGGGGATGATGACGTCTTGGACACAGACAAACATGTCTTCTAC 771
Qy 798 CTGCAAGACCATGACCTGCGCGCACCTTCTGTGGGCGACATGATCCAAAAGTGGGC 857
Db 772 CTGCAAGACCATGACCTGCGCGCACCTTCTGTGGGCGACATGATCCAAAAGTGGGC 831
Qy 858 CCCATCCGGGCTTTTGGAGCAAGTATGTGCGAGAGGTGTGACTCAAAATGAGCGG 917
Db 832 CCCATCCGGGCTTTTGGAGCAAGTATGTGCGAGAGGTGTGACTCAAAATGAGCGG 891
Qy 918 TACCCACCTATGTGGGGGGTGGTGGCTTCTGTGCTGCGGCTTCAACGGCGGTGCGCTG 977
Db 892 TACCCACCTATGTGGGGGGTGGTGGCTTCTGTGCTGCGGCTTCAACGGCGGTGCGCTG 951
Qy 978 CGCGGTGTGCGCCATGTCTTGGACATCTTCCCATTTGATGATGTCTTCTGGGTATGTGT 1037
Db 952 CGCGGTGTGCGCCATGTCTTGGACATCTTCCCATTTGATGATGTCTTCTGGGTATGTGT 1011
Qy 1038 CTGAGACTTGAAGGAGCTGAAAGCTGCTCCCAAGGGGATCCGACAGTGTGGCGTGGG 1097
Db 1012 CTGAGACTTGAAGGAGCTGAAAGCTGCTCCCAAGGGGATCCGACAGTGTGGCGTGGG 1071
Qy 1098 GCTTCATCGCAACACCGTCTCTCTTGGACCCCTGCTTCAACGAGACCTGCTGGTGGT 1157
Db 1072 GCTTCATCGCAACACCGTCTCTCTTGGACCCCTGCTTCAACGAGACCTGCTGGTGGT 1131
Qy 1158 CACCGCTTCTACCTTATGATGATGTCTCATGTGGGATGCGCTGAACCAAGCCCAACTC 1217
Db 1132 CACCGCTTCTACCTTATGATGATGTCTCATGTGGGATGCGCTGAACCAAGCCCAACTC 1191
Qy 1218 ACCTGGGCAATAGACACAGATCTTACTGATGACATCGGGTCCCGACGCTCTGGGCT 1277
Db 1192 ACCTGGGCAATAGACACAGATCTTACTGATGACATCGGGTCCCGACGCTCTGGGCT 1251
Qy 1278 CCGTTCAGAGGAAAGGGGCGACCTTCTCCCAAGAAAGTGAAGACCTTGGTGGTGG 1337
Db 1252 CCGTTCAGAGGAAAGGGGCGACCTTCTCCCAAGAAAGTGAAGACCTTGGTGGTGG 1311
Qy 1338 AGCATTAAGGAGAGTCCAGGGAAAGTGTGAAGTGTGAATATTCGTGCTGGCGAA 1397
Db 1312 AGCATTAAGGAGAGTCCAGGGAAAGTGTGAAGTGTGAATATTCGTGCTGGCGAA 1371
Qy 1398 CTCTTCAACATCTTCAAAACCAAGCTGTGATGATGATGATGATGATGATGATGATG 1457
Db 1372 CTCTTCAACATCTTCAAAACCAAGCTGTGATGATGATGATGATGATGATGATGATG 1431
Qy 1458 AGGAATCCAGAAATATGATCTTCTTTTGGGCTGAATGAGGAGAAAGTGGCTGTG 1517
Db 1432 AGGAATCCAGAAATATGATCTTCTTTTGGGCTGAATGAGGAGAAAGTGGCTGTG 1491
Qy 1518 TAGAGTTCAAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1577
Db 1492 TAGAGTTCAAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1551

Qy 1578 CACCTACTCAGACGGGATGCTTAAGCAGTGCACCTGAGTGTGTTAATGGCAGATPAAG 1637
Db 1552 CACCTACTCAGACGGGATGCTTAAGCAGTGCACCTGAGTGTGTTAATGGCAGATPAAG 1611
Qy 1638 TCCGTGTGAGTTCCAGGCGAGCCAGAACTCCTGTGTCCACATAGAGCTGAAGTGA 1697
Db 1612 TCCGTGTGAGTTCCAGGCGAGCCAGAACTCCTGTGTCCACATAGAGCTGAAGTGA 1671
Qy 1698 ATATCTTTCAAGCCAGAGAGAGGGTCTGATCTTAACCTTCTGAGTCTCAAGAA 1757
Db 1672 ATATCTTTCAAGCCAGAGAGAGGGTCTGATCTTAACCTTCTGAGTCTCAAGAA 1731
Qy 1758 CTGAGAAAGTTGGGGGATTAACAGAGAGTGTGGAATGGAACCGGCCCTCTTACTTG 1817
Db 1732 CTGAGAAAGTTGGGGGATTAACAGAGAGTGTGGAATGGAACCGGCCCTCTTACTTG 1791
Qy 1818 TGGGATCAAAATGCTGTAAATGTGAGAGTGTGGCAGAGAGGAGGCAAGTGTCTTGA 1877
Db 1792 TGGGATCAAAATGCTGTAAATGTGAGAGTGTGGCAGAGAGGAGGCAAGTGTCTTGA 1851
Qy 1878 AGTTGTGAGAGCTCAGAGTTTCTGGGCTCTCATTAAGAGCCCTCATTCCTGTTCCTC 1937
Db 1852 AGTTGTGAGAGCTCAGAGTTTCTGGGCTCTCATTAAGAGCCCTCATTCCTGTTCCTC 1911
Qy 1938 AAGAAATTCAGAGAACAGCATGCGGGGCTGGAATGATCTTTAATGGGCCAAAGGCAAG 1997
Db 1912 AAGAAATTCAGAGAACAGCATGCGGGGCTGGAATGATCTTTAATGGGCCAAAGGCAAG 1971
Qy 1998 CATATGCTCATCATGCTCTGAGAGAGAGAGATTCAAGTCTCTCAGAGCTCTCCTCA 2057
Db 1972 CATATGCTCATCATGCTCTGAGAGAGAGAGATTCAAGTCTCTCAGAGCTCTCCTCA 2031
Qy 2032 CCCAGATATGTTTACAGATTACGGGGGAGACCGGGTGAAGCATGACCCCTGACGCCCC 2091
Db 2118 AGCTTCAAGCTCAGAGTCTGCAAGTCAAGCTTCAAGGCAATGATGGGGAGGCTGG 2177
Qy 2092 AGCTTCAAGCTCAGAGTCTGCAAGTCAAGCTTCAAGGCAATGATGGGGAGGCTGG 2151
Db 2178 GGGAAATATAAATTTTGTGAAGA 2200
Db 2152 GGGAAATATAAATTTTGTGAAGA 2174

RESULT 4
US-10-205-890-287
; Sequence 287, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205, 890
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18

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; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 287
; LENGTH: 2210
; TYPE: DNA
; ORGANISM: Homo Sapien
; OS-10-205-890-287

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Query Match	96.1%	Score 2119.8	DB 13	Length 2210
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2121	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	78	GGAACCCCGCCAGAGAGCTCTCAAGGCCAACCCAGACCTGTGGCTGGCCAGATGAAGAT	137	
Db	52	GGAGCCCGCCAGAGAGCTCTCAAGGCCAACCCAGACCTGTGGCTGGCCAGATGAAGAT	111	
QY	138	CTCCGGCAACGGGGGAGCCCAATGCCACCTCAATCTGGCCATCGGCGCTTTCAACCTCTC	197	
Db	112	CTCCGGCAACGGGGGAGCCCAATGCCACCTCAATCTGGCCATCGGCGCTTTCAACCTCTC	171	
QY	198	CTCTTCAGTCGTAGTGTACACCAACCCACCTGGAAAGTCCAGAGACCAACCGGCATC	257	
Db	172	CTCTTCAGTCGTAGTGTACACCAACCCACCTGGAAAGTCCAGAGACCAACCGGCATC	231	
QY	258	CCCGAGGCCCTTGAGCTGGCCCACTCAACCAACCGCCAGACCCGGCCCGCTGCATGCC	317	
Db	232	CCCGAGGCCCTTGAGCTGGCCCACTCAACCAACCGCCAGACCCGGCCCGCTGCATGCC	291	
QY	318	AACACCTCTATAGTTCACCCACCCGCACTTGGCCACGACCGCCAGACAGTTCAAGATTCC	377	
Db	292	AACACCTCTATAGTTCACCCACCCGCACTTGGCCACGACCGCCAGACAGTTCAAGATTCC	351	
QY	378	CTCCGTGAACAGACACTGGCCGACACTTTCCCGCTGCAAGAGACGTGCCCCCTTAAGTGC	437	
Db	352	CTCCGTGAACAGACACTGGCCGACACTTTCCCGCTGCAAGAGACGTGCCCCCTTAAGTGC	411	
QY	438	GCGAGCCCGGTCTTCTGCTGCTGGTGTATCAAGTCTCCCTAGCAACTATATGTGGCGGC	497	
Db	412	GCGAGCCCGGTCTTCTGCTGCTGGTGTATCAAGTCTCCCTAGCAACTATATGTGGCGGC	471	
QY	498	GAGCTGCTGGCGGCGACGTGGGGCCGGAGCGCAAGGTAAGGGGTTTGCAGCTGGCTGC	557	
Db	472	GAGCTGCTGGCGGCGACGTGGGGCCGGAGCGCAAGGTAAGGGGTTTGCAGCTGGCTGC	531	
QY	558	CTCTTCCGGGGGACACAGCTCCAACCCGACAGAGCCCGCAAGTCAACCGGCTGGTG	617	
Db	532	CTCTTCCGGGGGACACAGCTCCAACCCGACAGAGCCCGCAAGTCAACCGGCTGGTG	591	
QY	618	GAGCTGAGGACACAGACTCAAGAGACATCTCGAGTGGGACTTCAAGACTCTCTTCTTC	677	
Db	592	GAGCTGAGGACACAGACTCAAGAGACATCTCGAGTGGGACTTCAAGACTCTCTTCTTC	651	
QY	678	AACCTCAAGCTCAAGACAGTCTGTCTTTCAGTGGCAGAGACAAAGGTGGCCAAAGCC	737	
Db	652	AACCTCAAGCTCAAGACAGTCTGTCTTTCAGTGGCAGAGACAAAGGTGGCCAAAGCC	711	
QY	738	AGCTTGGTGCACACGGGGATGAAGTCTTTTGACACACAGACAAATAGTCTTCTAC	797	
Db	712	AGCTTGGTGCACACGGGGATGAAGTCTTTTGACACACAGACAAATAGTCTTCTAC	771	

QY	798	TTGAGAGACATAGACCTGGCGCGCACCTCTTGTTGGGGCAATGATATCCAAAACGTGGGC	857
Db	772	CTGGAGACATAGACCTGGCGCGCACCTCTTGTTGGGGCAATGATATCCAAAACGTGGGC	831
QY	858	CCCATCCGGGCTTTTGGACCAAGTACTATGTGCGAAGGTGTGACTGAAATGACGG	917
Db	832	CCCATCCGGGCTTTTGGACCAAGTACTATGTGCGAAGGTGTGACTGAAATGACGG	891
QY	918	TACCAACCCATATGTGGGGGTGGTGGCTTTGCTGCTCCCGTTTCACGGCCGTGGCCG	977
Db	892	TACCAACCCATATGTGGGGGTGGTGGCTTTGCTGCTCCCGTTTCACGGCCGTGGCCG	951
QY	978	CGCCGCTCTGCCCATGTCTTGGACATCTTCCCATGATGATGTCTCCGTGGATATGT	1037
Db	952	CGCCGCTCTGCCCATGTCTTGGACATCTTCCCATGATGATGTCTCCGTGGATATGT	1011
QY	1038	CTGAGACTTGAAGGACTGAAGCTGCTCCACAGCGGATCCGACGTTGTGGCTGGCG	1097
Db	1012	CTGAGACTTGAAGGACTGAAGCTGCTCCACAGCGGATCCGACGTTGTGGCTGGCG	1071
QY	1098	GCTCATTCGGAACAACCTGTCTCTCTTGAACCCCTGTCTTACCCGAACCTGCGCTGGG	1157
Db	1072	GCTCATTCGGAACAACCTGTCTCTCTTGAACCCCTGTCTTACCCGAACCTGCGCTGGG	1131
QY	1158	CACCGCTTCTTACCTTATGAGATGCTCTCATGTGGATGCGGTGAACAGCCCAACCTC	1217
Db	1132	CACCGCTTCTTACCTTATGAGATGCTCTCATGTGGATGCGGTGAACAGCCCAACCTC	1191
QY	1218	ACCTGGCGGAATAGACACAGATCTTACTAGTCAGATATAGAGGTCCCGACCTTGGGCT	1277
Db	1192	ACCTGGCGGAATAGACACAGATCTTACTAGTCAGATATAGAGGTCCCGACCTTGGGCT	1251
QY	1278	CTGTGTTCCAGAGAAAGGGCGCACACCTTCTCTCCAGAAAGCTGAGACCTTTGTGGTCTG	1337
Db	1252	CTGTGTTCCATAGGAAGGGCGCACACCTTCTCTCCAGAAAGCTGAGACCTTTGTGGTCTG	1311
QY	1338	AGCATTAAGGAGTGCACGGGAGGTTTGAAGTTTGAATGATGAATATTCTGCTGGCGAA	1397
Db	1312	AGCATTAAGGAGTGCACGGGAGGTTTGAAGTTTGAATGATGAATATTCTGCTGGCGAA	1371
QY	1398	CTCCTACACATCCCTTAAAAACCACTCGGATCTGTTCCAGACATCTTCCCTGAGGCTGG	1457
Db	1372	CTCCTACACATCCCTTAAAAACCACTCGGATCTGTTCCAGACATCTTCCCTGAGTGGCTGG	1431
QY	1458	AGGAATCCGAAAAATATGATCTTCTTTTGTGTGCTGTAAATGCGAAGTCCGTGTC	1517
Db	1432	AGGAATCCGAAAAATATGATCTTCTTTTGTGTGCTGTAAATGCGAAGTCCGTGTC	1491
QY	1518	TAGAATTCGAACGTGTGATGCACTCCGCTCCGTTTGATGCAAGTCTTACTTCCCTGCTCT	1577
Db	1492	TAGAATTCGAACGTGTGATGCACTCCGCTCCGTTTGATGCAAGTCTTACTTCCCTGCTCT	1551
QY	1578	CACCTACTCAGACGGGATGCTTAACAGTGCACCTGCACTGAGTGGTTTAAATGCGAATTAAGC	1637
Db	1552	CACCTACTCAGACGGGATGCTTAACAGTGCACCTGCACTGAGTGGTTTAAATGCGAATTAAGC	1611
QY	1638	TCCGTCTGCACTTCCAGCGGACGCGCAGAACTCTGTGTCCACATAGAGCTTGAAGAA	1697
Db	1612	TCCGTCTGCACTTCCAGCGGACGCGCAGAACTCTGTGTCCACATAGAGCTTGAAGAA	1671
QY	1698	ATAATCTTTGAGCCCAAGAGAGAGGGTCCGATCTTAAACCTTTCTGGGTCTCAGACAA	1757
Db	1672	ATAATCTTTGAGCCCAAGAGAGAGGGTCCGATCTTAAACCTTTCTGGGTCTCAGACAA	1731
QY	1758	CTCAGAAAGTTGGGGGGATATCCAGAGAGTGTGTGAATAGAACCGGCCCTCTTACTTGG	1817
Db	1732	CTCAGAAAGTTGGGGGGATATCCAGAGAGTGTGTGAATAGAACCGGCCCTCTTACTTGG	1791
QY	1818	TGGGATCAAAATGCTGTAAATGTGTGAAGTGTGGGCAAGAGAGGCAAGTGTCTTTGAA	1877
Db	1792	TGGGATCAAAATGCTGTAAATGTGTGAAGTGTGGGCAAGAGAGGCAAGTGTCTTTGAA	1851

Qy	1878	AGTTGTAGACCTCAGAGTTTCTGGGGGCTCATTAGGAGCCCCATCCGTGTGTTCCC	1993
Dp	1852	AGTTGTAGACCTCAGAGTTTCTGGGGGCTCATTAGGAGCCCCATCCGTGTGTTCCC	1911
Qy	1938	AAGAATTCAGAGAACAGCACTGGGGGCTTGAATGATCTTAAATGGGCCCAAGCCAAACAGG	1997
Dp	1912	AAGAATTCAGAGAACAGCACTGGGGGCTTGAATGATCTTAAATGGGCCCAAGCCAAACAGG	1971
Qy	1998	CATATGCTCTCACTACTGCTGGAGAGGGAGATTCAGTCTCTTCACAGACCTTCCCTCA	2057
Dp	1972	CATATGCTCTCACTACTGCTGGAGAGGGAGATTCAGTCTCTTCACAGACCTTCCCTCA	2031
Qy	2058	CCCAGTATGTTTTCACAGATTACGGGGGGGACCGGGGTGAGCCAGTGACCCCTTCAGACCCCC	2117
Dp	2032	CCCAGTATGTTTTCACAGATTACGGGGGGGACCGGGGTGAGCCAGTGACCCCTTCAGACCCCC	2091
Qy	2118	AGCTTTCAGGCTCTCAGTGTCTGCCAGTCAAGCTTTCACAGGCAATTGTGATGGGGCAGCCTTG	2177
Dp	2092	AGCTTTCAGGCTCTCAGTGTCTGCCAGTCAAGCTTTCACAGGCAATTGTGATGGGGCAGCCTTG	2151
Qy	2178	GGGAATATAAATTTTGTGAAGA 2200	
Dp	2152	GGGAATATAAATTTTGTGAAGA 2174	

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RESULT 5
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; Sequence 287, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C538
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
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; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 287
; LENGTH: 2210
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-287

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Query Match	96.1%	Score 2119.8;	DB 13;	Length 2210;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 2121; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	78	GGAGCCGGCCCAAGGAGCTCTCCAGACGCAACCCAGACCTCTGGCTGGCCAGATGAATAT	137
Db	52	GGAGCCGGCCCAAGGAGCTCTCAAGCCGACCCCAAGACCTCTGGCTGGCCAGATGAATAT	111
QY	138	CTCCGGCAACGGGCGGGCCCAATGCCACCTCTATTTCTGGCATCTGGGCGCTTTACCTCTCC	197
Db	112	CTCCGGCAACGGGCGGGCCCAATGCCACCTCTATTTCTGGCATCTGGGCGCTTTACCTCTCC	171
QY	198	CTCTTTCAGTCTGCTAGTGTCAACAACAACCTGCAAGGTCCAGAGACAGCAACCGGCGATC	257
Db	172	CTCTTTCAGTCTGCTAGTGTCAACAACAACCTGCAAGGTCCAGAGACAGCAACCGGCGATC	231
QY	258	CCCGAAGCCCTTGGCTTGGCCCATCTCCACCAACCCGCCACGCCCCGGCTGCTCATGCC	317
Db	232	CCCGAAGCCCTTGGCTTGGCCCATCTCCACCAACCCGCCACGCCCCGGCTGCTCATGCC	291
QY	318	AACACCTTATAGTCAACCAACCCGGAATTGCGCAGCAGCCGACAGCATTTCAAACTTC	377
Db	292	AACACCTTATAGTCAACCAACCCGGAATTGCGCAGCAGCCGACAGCATTTCAAACTTC	351
QY	378	CTCCTGTACAGACACTGGCCGACATTTCCCTGCTGACAGACGTGCCCTCTTAATGTC	437
Db	352	CTCCTGTACAGACACTGGCCGACATTTCCCTGCTGACAGACGTGCCCTCTTAATGTC	411
QY	438	GCGCAGCCGGCTTCTCTGCTGCTGTGTAAAGTCTTCCCTTAGCACTATAGTGCGCGC	497
Db	412	GCGCAGCCGGCTTCTCTGCTGCTGTGTAAAGTCTTCCCTTAGCACTATAGTGCGCGC	471
QY	498	GAGCTGCTGCGGCGCACGTGGAGCGCGAGCGCAAGGTAACGGGTTTGACGTGCGCTC	557
Db	472	GAGCTGCTGCGGCGCACGTGGAGCGCGAGCGCAAGGTAACGGGTTTGACGTGCGCTC	531
QY	558	CTCTTCCGAGGAGGACACAGCCTCCAAACCGGACGAGGCGCGCAAGGTCACACGGCTGCTG	617
Db	532	CTCTTCCGAGGAGGACACAGCCTCCAAACCGGACGAGGCGCGCAAGGTCACACGGCTGCTG	591
QY	618	GAGCTGAGGACACAGACTCAACGAGAGACCTCTGAGTGGGACTTTCACAGACTCTTCTTC	677
Db	592	GAGCTGAGGACACAGACTCAACGAGAGACCTCTGAGTGGGACTTTCACAGACTCTTCTTC	651
QY	678	AACTCAACGCTCAAGCAGGTCCTGTCTTTCACAGGACGAGACAAAGGTGGCCAAACGCC	737
Db	652	AACTCAACGCTCAAGCAGGTCCTGTCTTTCACAGGACGAGACAAAGGTGGCCAAACGCC	711
QY	738	AGCTTCGTGTCAACGGGAGTATGATCGTCTTTGCACACACAGCAACATGATCTTCTAC	797
Db	712	AGCTTCGTGTCAACGGGAGTATGATCGTCTTTGCACACACAGCAACATGATCTTCTAC	771
QY	798	CTGACAGACCAATGACCTTGGCCGACACTCTTGGGGGCAACGTATTCAAAAGTGGGC	857
Db	772	CTGACAGACCAATGACCTTGGCCGACACTCTTGGGGGCAACGTATTCAAAAGTGGGC	831
QY	858	CCCATCCGGGCTTTTGGAGCAAGTACTATGTGCAAGGTGTGACTCAGAAATGAGCGG	917
Db	832	CCCATCCGGGCTTTTGGAGCAAGTACTATGTGCAAGGTGTGACTCAGAAATGAGCGG	891
QY	918	TACCCACCTTATTTGTGGGGGTGTGGCTTTTGCTGTCCGCTTCAAGGCGCTGGCCTG	977
Db	892	TACCCACCTTATTTGTGGGGGTGTGGCTTTTGCTGTCCGCTTCAAGGCGCTGGCCTG	951
QY	978	CGCGGTCTGCCCATGTCTTGGACATCTTCCCAATTATATATGTCTTCTGGGATATGAT	1037
Db	952	CGCGGTCTGCCCATGTCTTGGACATCTTCCCAATTATATATGTCTTCTGGGATATGAT	1011
QY	1038	CTGAGACTTGAAGGACTGAAGCTGCTCCCAACGCGCATCCGACGTCGTGGCGTGGCGG	1097
Db	1012	CTGAGACTTGAAGGACTGAAGCTGCTCCCAACGCGCATCCGACGTCGTGGGATGCGG	1071

QY 318 AACACCTTATGATGATCAACCCGAGCTTGCACAGAGCCGACAGCTTACAGAACTTC 377
Db 292 AACACCTTATGATGATCAACCCGAGCTTGCACAGAGCCGACAGCTTACAGAACTTC 351
QY 378 CTCTGTGACAGACAGCTGCGGCACTTTCCCTGCTGACAGAGCTGCGGCTTAACTGC 437
Db 352 CTCTGTGACAGACAGCTGCGGCACTTTCCCTGCTGACAGAGCTGCGGCTTAACTGC 411
QY 438 GCGAGCGGATCTTCCGCTGCTGATGATCAAGCTTCCCTTACAGCTTATGAGCGGCG 497
Db 412 GCGAGCGGATCTTCCGCTGCTGATGATCAAGCTTCCCTTACAGCTTATGAGCGGCG 471
QY 498 GAGCTGTGCGGACAGCTGCGGCGGAGCGCAAGGATGACGAGGCTTGGAGCTGCGCTC 557
Db 472 GAGCTGTGCGGACAGCTGCGGCGGAGCGCAAGGATGACGAGGCTTGGAGCTGCGCTC 531
QY 558 CTCTTCTGTGCGGACAGCTTCCACCCGACAGAGCCCGACAGGATGACCGGCTGCTG 617
Db 532 CTCTTCTGTGCGGACAGCTTCCACCCGACAGAGCCCGACAGGATGACCGGCTGCTG 591
QY 618 GAGCTGTGCGGACAGCTTCCACCCGACAGAGCTTCCGAGCTTCCGAGCTTCTTC 677
Db 592 GAGCTGTGCGGACAGCTTCCACCCGACAGAGCTTCCGAGCTTCCGAGCTTCTTC 651
QY 678 AACCTCAAGCTCAAGAGCTCTGTTCTTACAGTGCAGAGAGCAAGTGCAGAGCC 737
Db 652 AACCTCAAGCTCAAGAGCTCTGTTCTTACAGTGCAGAGAGCAAGTGCAGAGCC 711
QY 738 AGCTTGTGCTCAACGGGAGTATGACGTCTTTGACACACAGACCAATGCTTCTTAC 797
Db 712 AGCTTGTGCTCAACGGGAGTATGACGTCTTTGACACACAGACCAATGCTTCTTAC 771
QY 798 CTGAGAGACATGACCTGCGGCGCACCTGCTGCGGCGCAACGATCCAAAGCTGCGG 857
Db 772 CTGAGAGACATGACCTGCGGCGCACCTGCTGCGGCGCAACGATCCAAAGCTGCGG 831
QY 858 CCCATCGGAGCTTTTGGAGCAAGTATGATGACAGAGGCTGATCTCAAGATGAGCG 917
Db 832 CCCATCGGAGCTTTTGGAGCAAGTATGATGACAGAGGCTGATCTCAAGATGAGCG 891
QY 918 TACCCACCTTATGATGAGGAGTGTGCTTCTTGTCTGCTTCCGCTTACGCGCGCTGCG 977
Db 892 TACCCACCTTATGATGAGGAGTGTGCTTCTTGTCTGCTTCCGCTTACGCGCGCTGCG 951
QY 978 CGCGGTGCTGCGGATGCTTGAACATCTTCCCATGATGATGCTTCTGCGGATGATGCT 1037
Db 952 CGCGGTGCTGCGGATGCTTGAACATCTTCCCATGATGATGCTTCTGCGGATGATGCT 1011
QY 1038 CTGAGAGCTTGAAGAGCTGAGCTGCTCCACAGCGGATCCGACGCTGAGCGG 1097
Db 1012 CTGAGAGCTTGAAGAGCTGAGCTGCTCCACAGCGGATCCGACGCTGAGCGG 1071
QY 1098 GCTTCATCGGACAGCTGCTCTCTTGAACCCCTGCTTCAACGAGACCTGCTGCTG 1157
Db 1072 GCTTCATCGGACAGCTGCTCTCTTGAACCCCTGCTTCAACGAGACCTGCTGCTG 1131
QY 1158 CACCGCTTCTTACCTTATGAGATGCTGCTCATGATGAGATGCGCTGAACCGAGCCACCTC 1217
Db 1132 CACCGCTTCTTACCTTATGAGATGCTGCTCATGATGAGATGCGCTGAACCGAGCCACCTC 1191
QY 1218 ACCTGCGGCAATGAGACAGATCTACTGATGATGATGAGGATCCGAGCTTCTGAGCT 1277
Db 1192 ACCTGCGGCAATGAGACAGATCTACTGATGATGATGAGGATCCGAGCTTCTGAGCT 1251
QY 1278 CTGTGTTCCAGAGAGGCGGACACCTTCTCCAGAGAGCTGAGACCTTGTGTGCTG 1337
Db 1252 CTGTGTTCCAGAGAGGCGGACACCTTCTCCAGAGAGCTGAGACCTTGTGTGCTG 1311
QY 1338 AGCATTAAGGAGGCGGAGAGGATTTGAGATTTGAGATGATTTCTGCGTGGGAG 1397
Db 1312 AGCATTAAGGAGGCGGAGAGGATTTGAGATTTGAGATGATTTCTGCGTGGGAG 1371
QY 1398 CTCTTACACATCTTCAAAACCACTGATGCTTCAAGATCTTCTGAGATGCTG 1457

Db 1372 CTCTTACACATCTTCAAAACCACTGATGCTTCAAGATCTTCTGAGATGCTG 1431
QY 1458 AGGAATCTCGAATAATGATCTTCTTTTGTGCTGCTTAATGAGCAAGTGTGCTG 1517
Db 1432 AGGAATCTCGAATAATGATCTTCTTTTGTGCTGCTTAATGAGCAAGTGTGCTG 1491
QY 1518 TAGAGTTCAAGTGTGATGATCCGTCGCTTGTGAGTCAAAAGTCTTACTTCCCTGCT 1577
Db 1492 TAGAGTTCAAGTGTGATGATCCGTCGCTTGTGAGTCAAAAGTCTTACTTCCCTGCT 1551
QY 1578 CACCTACTCAAGAGGAGTCTTAAGCATGCACTTGCAGTGTGTTAATGACAGATTAAG 1637
Db 1552 CACCTACTCAAGAGGAGTCTTAAGCATGCACTTGCAGTGTGTTAATGACAGATTAAG 1611
QY 1638 TCCGTCTGCACTTCCAGGCGGACCAAGAACTCTGTGTCAATAGATGAGCTGAGAA 1697
Db 1612 TCCGTCTGCACTTCCAGGCGGACCAAGAACTCTGTGTCAATAGATGAGCTGAGAA 1671
QY 1698 ATATCTTCAAGCCAGGAGAGAGGAGTCTGATCTTAACCTTCTGAGCTTCAAGAA 1757
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Db 1732 CTGAGAGGATTTGGGAGGATACAGAGAGTGTGATTAAGAGCCGCTCTTACTTGG 1791
QY 1818 TGGATCAAAATGCTGTAATGATGATGATGAGGAGAGGAGGAGCAAGTGTCTTGA 1877
Db 1792 TGGATCAAAATGCTGTAATGATGATGATGAGGAGGAGGAGGAGCAAGTGTCTTGA 1851
QY 1878 AGTTGTGAGAGCTCAGAGTCTTGGGAGTCTCAATTAAGAGCCGCTCTGAGTCTG 1937
Db 1852 AGTTGTGAGAGCTCAGAGTCTTGGGAGTCTCAATTAAGAGCCGCTCTGAGTCTG 1911
QY 1938 AAGAAATTCAGAGAAACAGCACTGCGGCTGAGATGATCTTAATGAGGCGCAAGG 1997
Db 1912 AAGAAATTCAGAGAAACAGCACTGCGGCTGAGATGATCTTAATGAGGCGCAAGG 1971
QY 1998 CATATGCTCACTACGCTGCTGAGAGAGGAGAGATTCAGTCTCCAGAGCTCTCTCA 2057
Db 1972 CATATGCTCACTACGCTGCTGAGAGAGGAGAGATTCAGTCTCCAGAGCTCTCTCA 2031
QY 2058 CCCAGTATGTTTACAGATTAGCGGAGGAGCCGAGTGAAGCCGCTGAGAGCCG 2117
Db 2032 CCCAGTATGTTTACAGATTAGCGGAGGAGCCGAGTGAAGCCGCTGAGAGCCG 2091
QY 2118 AGCTTCAAGGCTCAGTGTGCTGAGTCAAGCTTCAAGGATGATGATGAGGAGCTT 2177
Db 2092 AGCTTCAAGGCTCAGTGTGCTGAGTCAAGCTTCAAGGATGATGATGAGGAGCTT 2151
QY 2178 GGGAAATATAAATTTTGTGAAGA 2200
Db 2152 GGGAAATATAAATTTTGTGAAGA 2174

RESULT 7
US-10-174-581-287
Sequence 287, Application US/10174581
Publication No. US20030017540A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C41
CURRENT APPLICATION NUMBER: US/10/174,581
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
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PRIOR FILING DATE: 1997-10-17
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 2 PRIOR FILING DATE: 1998-06-05
 3 PRIOR APPLICATION NUMBER: 60/088326
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 5 PRIOR APPLICATION NUMBER: 60/088655
 6 PRIOR FILING DATE: 1998-06-09
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 9 PRIOR APPLICATION NUMBER: 60/088738
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 27 PRIOR APPLICATION NUMBER: 60/089090
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 29 PRIOR APPLICATION NUMBER: 60/089105
 30 PRIOR FILING DATE: 1998-06-12
 31 PRIOR APPLICATION NUMBER: 60/089512
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 33 PRIOR APPLICATION NUMBER: 60/089514
 34 PRIOR FILING DATE: 1998-06-16
 35 PRIOR APPLICATION NUMBER: 60/089538
 36 PRIOR FILING DATE: 1998-06-17
 37 PRIOR APPLICATION NUMBER: 60/089598
 38 PRIOR FILING DATE: 1998-06-17
 39 PRIOR APPLICATION NUMBER: 60/089653

Query Match	Similarity	96.1%	Score 2119.8	DB 13	Length 2210
Best Local	Similarity	99.9%	Pred. No. 0		
Matches 2121	Conservative	0	Mismatches	2	Indels
		0	Gaps	0	
QY	78	GGAGCCGCCGAGAGCTCTCAAGGCCAGCCCGACAGCCCTGGCTGGCGAGATGAATAT	137		
Db	52	GGAGCCGCCGAGAGGCTCTCAAGGCCAGCCCGACAGCCCTGGCTGGCGAGATGAATAT	111		
QY	138	CTCCGGCAGCCGGCCGGCCCAATGCCACCTCAATTCGGGCATTCGGGGCTTCAACCTCTCTC	197		
Db	112	CTCCGGCAGCCGGCCGGCCCAATGCCACCTCAATTCGGGCATTCGGGGCTTCAACCTCTCTC	171		
QY	198	CTCTTCAGTCTGTAGTGTCAACCAACCACTGCAAGTTCAGAGACAGCAACCGGCAGATC	257		
Db	172	CTCTTCAGTCTGTAGTGTCAACCAACCACTGCAAGTTCAGAGACAGCAACCGGCAGATC	231		
QY	258	CCCGAGGCCCTTGGGCTTGGCCCACTTCACATCCACCGGCCAGGCCCGGCCCTTGCATATGC	317		
Db	232	CCCGAGGCCCTTGGGCTTGGCCCACTTCACATCCACCGGCCAGGCCCGGCCCTTGCATATGC	291		
QY	318	AACACCTTATAGTGTCAACCAACCGGACTTGGCGACGACGCGAGCAAGTTTCAGAACTTC	377		
Db	292	AACACCTTATAGTGTCAACCAACCGGACTTGGCGACGACGCGAGCAAGTTTCAGAACTTC	351		
QY	378	CTCTGTATCAGACACTGCGCGCACTTTTCCCTGTGACAGACGTGCCCCCTTAAGTGC	437		
Db	352	CTCTGTATCAGACACTGCGCGCACTTTTCCCTGTGACAGACGTGCCCCCTTAAGTGC	411		
QY	438	GGCGAGCCGGCTTCTCTGTGCTGGTGTATCAAGTCTCCCTAGCAACTATGTGGCGCGC	497		
Db	412	GGCGAGCCGGCTTCTCTGTGCTGGTGTATCAAGTCTCCCTAGCAACTATGTGGCGCGC	471		
QY	498	GAGCTGCTGGCGCGACGTGGAGCCCGGACGCGAAGTATCGAGGTTTTCAGCTGCGCTCTC	557		

Db	472	GAGCTGCTGCGCGCAACCTGGGGCCGCCAGCGAAGTACGGGGTTTGCACTGGCGCTC	531
Qy	558	CTCTTCTGTGTGGGCAAGCCTTCCAACCGACAGGCCCGCAAGTCAACCGCTGCTG	617
Db	532	CTCTTCTGTGTGGGCAAGCCTTCCAACCGACAGGCCCGCAAGTCAACCGCGTGGCTG	591
Qy	618	GAGCTGAGGCAACAGCTCACGGAGACATCTCTGAGTGGGACTTCCAGACTCTCTTCTTC	677
Db	592	GAGCTGAGGCAACAGCTCACGGAGACATCTCTGAGTGGGACTTCCAGACTCTCTTCTTC	651
Qy	678	AACCTCAAGCTCAAGCAGAGTCTGTCTTCAAGTGGCAGAGACAAGGTGCGCCAAAGCC	737
Db	652	AACCTCAAGCTCAAGCAGAGTCTGTCTTCAAGTGGCAGAGACAAGGTGCGCCAAAGCC	711
Qy	738	AGCTTCGTGCTCAACGGGGATGATGACGTCTTTTGACAACAAGACAATGGTCTTCTAC	797
Db	712	AGCTTCGTGCTCAACGGGGATGATGACGTCTTTTGACAACAAGACAATGGTCTTCTAC	771
Qy	798	CTGCAAGAACATGACCTCTGGCCGCCACTCTTCGTGGGGCAACTGATCCAAAGTGGGG	857
Db	772	CTGCAAGAACATGACCTCTGGCCGCCACTCTTCGTGGGGCAACTGATCCAAAGTGGGG	831
Qy	858	CCCAATCCGGGGCTTTTGGAGCAAGTATATGACAGAGGTGTGACTCAGATATGAGCGG	917
Db	832	CCCAATCCGGGGCTTTTGGAGCAAGTATATGACAGAGGTGTGACTCAGATATGAGCGG	891
Qy	918	TACCCACCCCTATTTGTGGGGGTGTGGCTTCTTGGCTGCTCCGCTTCAACGGCGCTGCGCTG	977
Db	892	TACCCACCCCTATTTGTGGGGGTGTGGCTTCTTGGCTGCTCCGCTTCAACGGCGCTGCGCTG	951
Qy	978	CGCGGTGCTGCCCATGTCTTGTGACATCTTCCCATTTGATGATGTCTTCTTGGGATGTGT	1037
Db	952	CGCGGTGCTGCCCATGTCTTGTGACATCTTCCCATTTGATGATGTCTTCTTGGGATGTGT	1011
Qy	1038	CTGAGAGCTTGAAGGAGCTGAAAGCTGCGCTCCACAAGCGGCATCCGACGTCGCGGTGGG	1097
Db	1012	CTGAGAGCTTGAAGGAGCTGAAAGCTGCGCTCCACAAGCGGCATCCGACGTCGCGGTGGG	1077
Qy	1098	GCTCCATGCAACAACCTGTCTCTCTTTGACCCCTGCTTCTACCGAGA CTTGTGCTGTG	1157
Db	1072	GCTCCATGCAACAACCTGTCTCTCTTTGACCCCTGCTTCTACCGAGA CTTGTGCTGTG	1137
Qy	1158	CACCGCTTCTTACCTTATGAGATGCTGCTCATGTGTGGATGCGCTGAACCAAGCCCACTC	1217
Db	1132	CACCGCTTCTTACCTTATGAGATGCTGCTCATGTGTGGATGCGCTGAACCAAGCCCACTC	1197
Qy	1218	AACGTGGGCATTCAGACACAGATCTACGTAGTCAAGATCAAGGTGCCAAGCTCTGGGCT	1277
Db	1192	AACGTGGGCATTCAGACACAGATCTACGTAGTCAAGATCAAGGTGCCAAGCTCTGGGCT	1257
Qy	1278	CCTGTTTTCAGAGGAAGGGGCGACACTTCTCTCCAGAGACTGAGACTTGTGTGTGCTG	1337
Db	1252	CCTGTTTTCAGAGGAAGGGGCGACACTTCTCTCCAGAGACTGAGACTTGTGTGTGCTG	1311
Qy	1338	AGCATTAAGGAGTGCACAGGAAGGTTTGATGAGTTGATGAGTAATTTCTGGCTGGCGAA	1397
Db	1312	AGCATTAAGGAGTGCACAGGAAGGTTTGATGAGTTGATGAGTAATTTCTGGCTGGCGAA	1377
Qy	1398	CTCTTACACATCTTCAAAACCCACCTGTGTACTGTTCCAGACATCTTCCCTGGATGGCTGG	1457
Db	1372	CTCTTACACATCTTCAAAACCCACCTGTGTACTGTTCCAGACATCTTCCCTGGATGGCTGG	1433
Qy	1458	AGGAATCCAGAAAAATATGATCTTCTTTTGTGGTCTTAATGGCAGAAAGTGCCTGTGCT	1517
Db	1432	AGGAATCCAGAAAAATATGATCTTCTTTTGTGGTCTTAATGGCAGAAAGTGCCTGTGCT	1497
Qy	1518	TAGAGTTCCAACTGTGATGTCATCCGTCCGTTTGAATCAAAAGTCTTACTTCCCTGCTCT	1577
Db	1492	TAGAGTTCCAACTGTGATGTCATCCGTCCGTTTGAATCAAAAGTCTTACTTCCCTGCTCT	1557
Qy	1578	CACCTTCTCACAGACGGGATGCTTAAGCAGTGCACCTGCAATGTGTTTAATGCAAGTAAGC	1637

Db 1552 CACCTACTCAGACGGGATGCTAAGCAGTCACTGCACTGGTTTAATGCGATTAAGC 1611
Qy 1638 TCCGCTGCACTTCCAGGCGCAGCAAACTCCTGTCATAGAGCTGAAGTGAAGA 1697
Db 1612 TCCGCTGCACTTCCAGGCGCAGCAAACTCCTGTCATAGAGCTGAAGTGAAGA 1671
Qy 1698 AATCTTTTCAGCCCAAGAGAGAGGGTCTGATCTTAACTCTTCTGAGTCTCAGACAA 1757
Db 1672 AATCTTTTCAGCCCAAGAGAGAGGGTCTGATCTTAACTCTTCTGAGTCTCAGACAA 1731
Qy 1758 CTGAGAGAGTTGGGGGGATACAGAGAGTGTGTGAATAGAACCCGCCCTCTTACTTG 1817
Db 1732 CTGAGAGAGTTGGGGGGATACAGAGAGTGTGTGAATAGAACCCGCCCTCTTACTTG 1791
Qy 1818 TGGGATCAAAATGCTGTATATGATGATGATGATGATGATGATGATGATGATGATGAT 1877
Db 1792 TGGGATCAAAATGCTGTATATGATGATGATGATGATGATGATGATGATGATGATGAT 1851
Qy 1878 AGTTGTAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGCCGCCATCCCTGTCTCC 1937
Db 1852 AGTTGTAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGCCGCCATCCCTGTCTCC 1911
Qy 1938 AAGAAATTCAGAGACAGCACTGGGCTGGAATGATCTTTAATGAGGCCAAGCCAAAG 1997
Db 1912 AAGAAATTCAGAGACAGCACTGGGCTGGAATGATCTTTAATGAGGCCAAGCCAAAG 1971
Qy 1998 CATATGCTCACTACTGCTCTGAGAGAGAGATTCAGAGTCTCCAGAGCTCCCTCA 2057
Db 1972 CATATGCTCACTACTGCTCTGAGAGAGAGATTCAGAGTCTCCAGAGCTCCCTCA 2031
Qy 2058 CCCAGATATTTTACAGATTAAGGGGGGACCGGGTGAAGCCAGTGAAGCCCTGCAAGCCCC 2117
Db 2032 CCCAGATATTTTACAGATTAAGGGGGGACCGGGTGAAGCCAGTGAAGCCCTGCAAGCCCC 2091
Qy 2118 AGCTTCAGGCTCAGAGTCTGCAAGTCAAGCTTCAACAGCAATTTGATGAGGCAAGCTTG 2177
Db 2092 AGCTTCAGGCTCAGAGTCTGCAAGTCAAGCTTCAACAGCAATTTGATGAGGCAAGCTTG 2151
Qy 2178 GGGAAATATAAATTTTGTGAAGA 2200
Db 2152 GGGAAATATAAATTTTGTGAAGA 2174

RESULT 8
US-10-176-483-287
Sequence 287, Application US/10176483
Publication No. US20030017541A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P34301C68
CURRENT APPLICATION NUMBER: US/10/176,483
Prior application removed - 2002-06-20
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 287
LENGTH: 2210
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-483-287

Query Match 96.1%; Score 2119.8; DB 13; Length 2210;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 78 GGAAGCCGCCAGAGAGCTCTCAGGCGCAAGCCAGACCTTGCTGGCCAGATGAAGTAT 137
Db 52 GGAAGCCGCCAGAGAGCTCTCAGGCGCAAGCCAGACCTTGCTGGCCAGATGAAGTAT 111
Qy 138 CTCGGGCAACGGGCGGCCAATGCAAGCCCAATTCCTGGGCAATGGGGCTTTTCAACCTCTC 197
Db 112 CTCGGGCAACGGGCGGCCAATGCAAGCCCAATTCCTGGGCAATGGGGCTTTTCAACCTCTC 171
Qy 198 CTCTTCAGTCTGTAGTGTACACCACTGCTGCAAGTCTCAGAGACAGCCAGCCGAGATC 257
Db 172 CTCTTCAGTCTGTAGTGTACACCACTGCTGCAAGTCTCAGAGACAGCCAGCCGAGATC 231
Qy 258 CCCGAGGCCCTGGCTGGCCCACTTCACCAACCGGCCAGCCCGGCCCGTGCATGCC 317
Db 232 CCCGAGGCCCTGGCTGGCCCACTTCACCAACCGGCCAGCCCGGCCCGTGCATGCC 291
Qy 318 AACACCTCTATGATGATCAACCCGGAATTTGGCAAGCCGCGGCAAGTTCAGAACTTC 377
Db 292 AACACCTCTATGATGATCAACCCGGAATTTGGCAAGCCGCGGCAAGTTCAGAACTTC 351
Qy 378 CTCTGTACAGACACTGCGCCACTTTCCCTGCTGCAAGACGTGCCCCCTCTTAAGTGC 437
Db 352 CTCTGTACAGACACTGCGCCACTTTCCCTGCTGCAAGACGTGCCCCCTCTTAAGTGC 411
Qy 438 GCGCAGCGGCTCTCTGCTGCTGTATCAAGTCTCTCCCTAGCAATATGAGCGCC 497
Db 412 GCGCAGCGGCTCTCTGCTGCTGTATCAAGTCTCTCCCTAGCAATATGAGCGCC 471
Qy 498 GAGCTGCTGCGCGCAGTGGGGCCGAGAGGCAAGGATCGGGTTTGGACGTGCGCTC 557
Db 472 GAGCTGCTGCGCGCAGTGGGGCCGAGAGGCAAGGATCGGGTTTGGACGTGCGCTC 531
Qy 558 CTCTTCTGTGTGGCAAGCTTCCAAACCCGCAAGAGCCGCAAGTCAACCGGCTGCTG 617
Db 532 CTCTTCTGTGTGGCAAGCTTCCAAACCCGCAAGAGCCGCAAGTCAACCGGCTGCTG 591
Qy 618 GAGCTGAGAGCAAGACTCAAGAGAGACATCTGCAAGTGGGCACTTCCAGATCTCTTCTC 677
Db 592 GAGCTGAGAGCAAGACTCAAGAGAGACATCTGCAAGTGGGCACTTCCAGATCTCTTCTC 651
Qy 678 AACCTCAGCTCAGACAGGTCTCTTCTTACAGTGGCAGAGACAAAGTGGCCAGCC 737
Db 652 AACCTCAGCTCAGACAGGTCTCTTCTTACAGTGGCAGAGACAAAGTGGCCAGCC 711
Qy 738 AGCTTGTGTCTCAACGGGATGATGACGTCTTTGCAACACAGCAACATGCTTCTAC 797
Db 712 AGCTTGTGTCTCAACGGGATGATGACGTCTTTGCAACACAGCAACATGCTTCTAC 771
Qy 798 CTGAGAGACCAATGACCTTGGCGCCGCACTTCTGCTGGGGCAATGATCCAAAGTGGGC 857
Db 772 CTGAGAGACCAATGACCTTGGCGCCGCACTTCTGCTGGGGCAATGATCCAAAGTGGGC 831
Qy 858 CCCATCCGGGGCTTTTGGAGCAAGTACTATGTGCAAGGTGGACTCAGAAATGAGCGG 917
Db 832 CCCATCCGGGGCTTTTGGAGCAAGTACTATGTGCAAGGTGGACTCAGAAATGAGCGG 891
Qy 918 TACCAACCTATTTGTGGGGGTGTGAGTCTTGTGCTTCCGCTTCAAGGCGGCTGCC 977
Db 892 TACCAACCTATTTGTGGGGGTGTGAGTCTTGTGCTTCCGCTTCAAGGCGGCTGCC 951
Qy 978 GCGCGTGTGCGCAATGTCTTGGAGACATCTTCCCAATGATATGATCTTCCGCTGATGT 1037
Db 952 GCGCGTGTGCGCAATGTCTTGGAGACATCTTCCCAATGATATGATCTTCCGCTGATGT 1011
Qy 1038 CTGAGCTTGAAGGAGCTGAAGCTGCTCCCAAGCGGCAATCCGCAAGTCTGAGGTGCGG 1097
Db 1012 CTGAGCTTGAAGGAGCTGAAGCTGCTCCCAAGCGGCAATCCGCAAGTCTGAGGTGCGG 1071
Qy 1098 GCTTCATGCAACACTGTCTCTCTTGTGACCCCTGCTTACCGAGACTGTGCTGTG 1157

Db 592 GAGCTGAGGAGACAGACTCAAGAGACATCTGAGTGGGACTTCCAGCACTCTTCTTC 651
QY 678 AACCTCAACGCTCAAGAGAGTCTGTTTACAGTGGCAGAGACAAGTGGCCCAAGCC 737
Db 652 AACCTCAACGCTCAAGAGAGTCTGTTTACAGTGGCAGAGACAAGTGGCCCAAGCC 711
QY 738 AGCTTCGTGCTCAACGGGAGTGAATGAGTCTTGGCACAAGACAAGATGCTTCTAC 797
Db 712 AGCTTCGTGCTCAACGGGAGTGAATGAGTCTTGGCACAAGACAAGATGCTTCTAC 771
QY 798 CTGAGAGACCATGACCTTGGCCGACCTTCTGTTGGGCACTGATCCAAAAGTGGC 857
Db 772 CTGAGAGACCATGACCTTGGCCGACCTTCTGTTGGGCACTGATCCAAAAGTGGC 831
QY 858 CCCATCCGGGCTTTTGGAGCAGTACTATGTCAGAGGTGTGACTCAGAAATGAGCCG 917
Db 832 CCCATCCGGGCTTTTGGAGCAGTACTATGTCAGAGGTGTGACTCAGAAATGAGCCG 891
QY 918 TACCAACCTTATGTTGGGGTGGTGGCTTCTGCTCCGCTTCAAGGCGGCTGACCTG 977
Db 892 TACCAACCTTATGTTGGGGTGGTGGCTTCTGCTCCGCTTCAAGGCGGCTGACCTG 951
QY 978 CGCCGTGCTGCCATGTTTGAACATCTTCCCATGATGATGCTTCTGGGTATGT 1037
Db 952 CGCCGTGCTGCCATGTTTGAACATCTTCCCATGATGATGCTTCTGGGTATGT 1011
QY 1038 CTGAGACTTGAAGGAGCTGAAGCTGCTCCACAGGGGATCCGACGCTGGCCGCG 1097
Db 1012 CTGAGACTTGAAGGAGCTGAAGCTGCTCCACAGGGGATCCGACGCTGGCCGCG 1071
QY 1098 GCTTCATCGCAACCTGTCTCTTGAACCCCTGCTTACCGAGACCTGCTGCTGTG 1157
Db 1072 GCTTCATCGCAACCTGTCTCTTGAACCCCTGCTTACCGAGACCTGCTGCTGTG 1131
QY 1158 CACCGCTTCTACCTTATGATGATGCTGCTCAATGTTGAGTGGATCCGTCAGACCAAGCCCTC 1217
Db 1132 CACCGCTTCTACCTTATGATGATGCTGCTCAATGTTGAGTGGATCCGTCAGACCAAGCCCTC 1191
QY 1218 ACTCGGGGCAATCAGACAGATCTTACTGATCAGATCAGAGGTCCCGACCTGGGGT 1277
Db 1192 ACTCGGGGCAATCAGACAGATCTTACTGATCAGATCAGAGGTCCCGACCTGGGGT 1251
QY 1278 CTTGTTTCAAGAGAAAGGGGCGACCTTCTCTCCAGAAAGCTGAGACCTTGTGTGTG 1337
Db 1252 CTTGTTTCAAGAGAAAGGGGCGACCTTCTCTCCAGAAAGCTGAGACCTTGTGTGTG 1311
QY 1338 AGCATTAAGGAGTGGCAGGAAAGTTTGAAGTTTGAATGATGATTAATTTGTGCTGCCAA 1397
Db 1312 AGCATTAAGGAGTGGCAGGAAAGTTTGAAGTTTGAATGATGATTAATTTGTGCTGCCAA 1371
QY 1398 CTCTTACACATCTTCAAAACCACCTGTGACTGTTCCAGCATCTTCCCTGGATGGCTGG 1457
Db 1372 CTCTTACACATCTTCAAAACCACCTGTGACTGTTCCAGCATCTTCCCTGGATGGCTGG 1431
QY 1458 AGGAATCCAGAAATATGATCTTCTTTTGTGCTGTAAATGGCAGAAAGTGGCTGTGC 1517
Db 1432 AGGAATCCAGAAATATGATCTTCTTTTGTGCTGTAAATGGCAGAAAGTGGCTGTGC 1491
QY 1518 TAGAGTTCAACTGTGATGATGATCCGCTCCGTTTGAAGTCAAGTCTTACCTCCGCTCT 1577
Db 1492 TAGAGTTCAACTGTGATGATGATCCGCTCCGTTTGAAGTCAAGTCTTACCTCCGCTCT 1551
QY 1578 CACCTTACTACAGACGGGATGCTAAAGTGAAGTGAAGTGGTAAATGGCAGATAAGC 1637
Db 1552 CACCTTACTACAGACGGGATGCTAAAGTGAAGTGAAGTGGTAAATGGCAGATAAGC 1611
QY 1638 TCCGCTCAGATTCAGGCGCAGGCAAAATCTGTGTCCACATGAGCTGACGTGAGAA 1697
Db 1612 TCCGCTCAGATTCAGGCGCAGGCAAAATCTGTGTCCACATGAGCTGACGTGAGAA 1671
QY 1698 ATATCTTTCAGGCCAGAGAGAGGGGTCTGATCTTAAACCTTTCTGAGCTCAGACAA 1757
Db 1672 ATATCTTTCAGGCCAGAGAGAGGGGTCTGATCTTAAACCTTTCTGAGCTCAGACAA 1731

QY 1758 CTCAGAGGTTGGGGAGATACCAGAGAGTGTGAAATAGAACCGCCCTCTCTACTTGG 1817
Db 1732 CTCAGAGGTTGGGGAGATACCAGAGAGTGTGAAATAGAACCGCCCTCTCTACTTGG 1791
QY 1818 TGGGATCAAAAGCTTAAATGTGTGAGTGTGTGGCAGAGAGAGGCAAGTCTTTGAA 1877
Db 1792 TGGGATCAAAAGCTTAAATGTGTGAGTGTGTGGCAGAGAGAGGCAAGTCTTTGAA 1851
QY 1878 AGTTGTGAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGGCCCATCCCTGTGTTCCC 1937
Db 1852 AGTTGTGAGAGCTCAGAGTTTCTGGGGTCTCATTTAGAGGCCCATCCCTGTGTTCCC 1911
QY 1938 AAGAAATCAGAGACAGCACTGGGGCTGAAATGATCTTAAATGGGCCCAAGCCAAAG 1997
Db 1912 AAGAAATCAGAGACAGCACTGGGGCTGAAATGATCTTAAATGGGCCCAAGCCAAAG 1971
QY 1998 CATATGCTCACTACTGCTGAGAGAGGAGATTCAGAGTCTCCAGACGCTCCCTCA 2057
Db 1972 CATATGCTCACTACTGCTGAGAGAGGAGATTCAGAGTCTCCAGACGCTCCCTCA 2031
QY 2058 CCCAGTATGTTTACAGATTAAGGGGAGACCGGGTGAAGCCAGTACCCCTGACAGCCCC 2117
Db 2032 CCCAGTATGTTTACAGATTAAGGGGAGACCGGGTGAAGCCAGTACCCCTGACAGCCCC 2091
QY 2118 AGCTTCAGGCTCAGGTCTGCTGCTGCTCAAGCTTCAAGGCAATGTGATGGGCAAGCTTGG 2177
Db 2092 AGCTTCAGGCTCAGGTCTGCTGCTGCTCAAGCTTCAAGGCAATGTGATGGGCAAGCTTGG 2151
QY 2178 GGAATATTAATTTTGGAGAA 2200
Db 2152 GGAATATTAATTTTGGAGAA 2174

RESULT 10
US-10-176-914-287
; Sequence 287, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Dian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; PRIORITY FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 287
; LENGTH: 2210
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-914-287

Query Match 96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 78 GGAAGCCGCGGAGAGGCTCTCAGGCGGAGCCGAGACCTGAGTGGCAGAAATGAAATG 137
Db 52 GGAAGCCGCGGAGAGGCTCTCAGGCGGAGCCGAGACCTGAGTGGCAGAAATGAAATG 111
QY 138 CTCGGGACCGGCGGCGCCAAATGCACTTCAATTTGCGCATGGCGCTTTCACCTCTTC 197

Db 112 CTCGGGACCGGGGCCCAATGCCACCCCTCATCTTGGCATCGGCGCTTTACCCCTCTC 171
QY CTCTTAGTGTGATGATGATCACCACCACTGCAAGGTCCAGAGAGCAGCCACGGGAGTC 257
Db 172 CTCTTAGTGTGATGATGATCACCACCACTGCAAGGTCCAGAGAGCAGCCACGGGAGTC 231
QY 258 CCGGAGCCCTGGCTGGCCCACTCCACCCACCGCCCAAGCCCGGCGCCGTCATGCC 317
Db 232 CCGGAGCCCTGGCTGGCCCACTCCACCCACCGCCCAAGCCCGGCGCCGTCATGCC 291
QY 318 AACACTCTATGGTCAACCCACCCGGAATTGGCCACGACCGGACGACGCTTCAAGATTC 377
Db 292 AACACTCTATGGTCAACCCACCCGGAATTGGCCACGACCGGACGACGCTTCAAGATTC 351
QY 378 CTCTTAGTGTGATGATGATCACCACCACTGCAAGGTCCAGAGAGCAGCCACGGGAGTC 437
Db 352 CTCTTAGTGTGATGATGATCACCACCACTGCAAGGTCCAGAGAGCAGCCACGGGAGTC 411
QY 438 GCGCAGCCGGTCTTCTGCTGTGTGATCAAGTCTCCCTAGCACTATGTGCGCGC 497
Db 412 GCGCAGCCGGTCTTCTGCTGTGTGATCAAGTCTCCCTAGCACTATGTGCGCGC 471
QY 498 GAGCTGCTGGCGGCAAGTGGGCGCGGAGCGCAAGGTACGGGGTTTGCAGTGGCGCTC 557
Db 472 GAGCTGCTGGCGGCAAGTGGGCGCGGAGCGCAAGGTACGGGGTTTGCAGTGGCGCTC 531
QY 558 CTCTTAGTGTGATGATGATCACCACCACTGCAAGGTCCAGAGAGCAGCCACGGGAGTC 617
Db 532 CTCTTAGTGTGATGATGATCACCACCACTGCAAGGTCCAGAGAGCAGCCACGGGAGTC 591
QY 618 GAGCTGAGGACAGACTCAGGAGACATCTGCAAGGTGAGCTTCCAGATCTCTTCTTC 677
Db 592 GAGCTGAGGACAGACTCAGGAGACATCTGCAAGGTGAGCTTCCAGATCTCTTCTTC 651
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Db 652 AACCTCAAGCTCAAGAGAGTCTGTCTTCAAGTGGCAGGACCAAGTGGCGCAAGGCC 711
QY 738 AGCTTGTGTCTCAACGGGAGTATGATGATCTTGGCAACAACAACAATGATCTTCTAC 797
Db 712 AGCTTGTGTCTCAACGGGAGTATGATGATCTTGGCAACAACAACAATGATCTTCTAC 771
QY 798 CTGAGAGACCATGACCTGGCGGCACTCTGCTGGGGGCACTGATCCAAAAGTGGGC 857
Db 772 CTGAGAGACCATGACCTGGCGGCACTCTGCTGGGGGCACTGATCCAAAAGTGGGC 831
QY 858 CCCATCCGGGCTTTTGGAGCAAGTATGATGACGAGAGTGTGATCTCAGAAATGACGG 917
Db 832 CCCATCCGGGCTTTTGGAGCAAGTATGATGACGAGAGTGTGATCTCAGAAATGACGG 891
QY 918 TACCCACCTATGTTGGGGGTGTGGCTTGTGCTGTCCGGCTTACGGCCGCTGCCCTG 977
Db 892 TACCCACCTATGTTGGGGGTGTGGCTTGTGCTGTCCGGCTTACGGCCGCTGCCCTG 951
QY 978 CGCGGTGCTGCATGCTTGGACATCTTCCCATTTGATGATGATCTTCTGGGATGATGT 1037
Db 952 CGCGGTGCTGCATGCTTGGACATCTTCCCATTTGATGATGATCTTCTGGGATGATGT 1011
QY 1038 CTGAGAGTGTGAGGAGTGAAGCTGCTCCCAACGCGGACATCCGAGTGTGGCGTGG 1097
Db 1012 CTGAGAGTGTGAGGAGTGAAGCTGCTCCCAACGCGGACATCCGAGTGTGGCGTGG 1071
QY 1098 GCTGCATGCAACCTGTCTCTCTTGTGACCCCTGCTTCAACGAGACTGTGCTGGTG 1157
Db 1072 GCTGCATGCAACCTGTCTCTCTTGTGACCCCTGCTTCAACGAGACTGTGCTGGTG 1131
QY 1158 CACCGCTTCTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1217
Db 1132 CACCGCTTCTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1191
QY 1218 ACCTGGGCAATGACACAGATCTTACTGATGATGATGATGATGATGATGATGATGATG 1277
Db 1192 ACCTGGGCAATGACACAGATCTTACTGATGATGATGATGATGATGATGATGATGATG 1251

QY 1278 CTTGTTTCCAGAGAGAGGCGACACCTTCTTCCAGAGAGTGAAGCTTTGTGTCTG 1337
Db 1252 CTTGTTTCCAGAGAGAGGCGACACCTTCTTCCAGAGAGTGAAGCTTTGTGTCTG 1311
QY 1338 AGCATTAAGGAGTGCAGGAGAGGTTTGAAGTGTGATGATGATGATGATGATGATGATG 1397
Db 1312 AGCATTAAGGAGTGCAGGAGAGGTTTGAAGTGTGATGATGATGATGATGATGATGATG 1371
QY 1398 CTCTTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1457
Db 1372 CTCTTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1431
QY 1458 AGGAACTCCAGAAATATGATCTTCTTTTGTGAGTCTTATATGAGAGAGTGTGCTG 1517
Db 1432 AGGAACTCCAGAAATATGATCTTCTTTTGTGAGTCTTATATGAGAGAGTGTGCTG 1491
QY 1518 TAGAGTTCCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1577
Db 1492 TAGAGTTCCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1551
QY 1578 CACTTACTCAGACGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1637
Db 1552 CACTTACTCAGACGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1611
QY 1638 TCCGTCTGAGTCTCAGAGGCGAGCAAGAACTCCGTGTGATGATGATGATGATGATG 1697
Db 1612 TCCGTCTGAGTCTCAGAGGCGAGCAAGAACTCCGTGTGATGATGATGATGATGATG 1671
QY 1698 ATATCTTTCAGCCAGAGAGAGAGGAGTCTGATCTTAAACCTTCTGAGTCTTCAACA 1757
Db 1672 ATATCTTTCAGCCAGAGAGAGAGGAGTCTGATCTTAAACCTTCTGAGTCTTCAACA 1731
QY 1758 CTGAGAGGTTGGGGGATTCAGAGAGTGTGATGATGATGATGATGATGATGATGATG 1817
Db 1732 CTGAGAGGTTGGGGGATTCAGAGAGTGTGATGATGATGATGATGATGATGATGATG 1791
QY 1818 TGGGATCAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1877
Db 1792 TGGGATCAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1851
QY 1878 AGTTGTGAGAGCTCAGAGTCTTGGGGTCTCTATTAAGAGACCCCATCCCTGTGCTCC 1937
Db 1852 AGTTGTGAGAGCTCAGAGTCTTGGGGTCTCTATTAAGAGACCCCATCCCTGTGCTCC 1911
QY 1938 AAGAAATCAGAGAACAGCACTGGGGCTGGAATGATCTTAAATGGGCCCAAGGCCAAG 1997
Db 1912 AAGAAATCAGAGAACAGCACTGGGGCTGGAATGATCTTAAATGGGCCCAAGGCCAAG 1971
QY 1998 CATATGCTTCACTATGCTCTGAGAGAGAGAGATTCAGGTCTCCAGAGAGCTCCCTCA 2057
Db 1972 CATATGCTTCACTATGCTCTGAGAGAGAGAGATTCAGGTCTCCAGAGAGCTCCCTCA 2031
QY 2058 CCCAGTATGTTTAAAGATTAAGAGGAGGAGCCGGGTGAGCAGTGAACCCCTGACGCC 2117
Db 2032 CCCAGTATGTTTAAAGATTAAGAGGAGGAGCCGGGTGAGCAGTGAACCCCTGACGCC 2091
QY 2118 AGCTTCAAGGCTCAGTGTCTGCAATCAAGCTTCAACAGGATGTGATGAGGAGCTTG 2177
Db 2092 AGCTTCAAGGCTCAGTGTCTGCAATCAAGCTTCAACAGGATGTGATGAGGAGCTTG 2151
QY 2178 GGGAAATTAATAATTTGTGAAGA 2200
Db 2152 GGGAAATTAATAATTTGTGAAGA 2174

RESULT 11

US-10-176-915-287
; Sequence 287, Application US/10176915
; Publication No. US2003017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3450R1C110
CURRENT APPLICATION NUMBER: US/10/176,915
PRIORITY FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 287
LENGTH: 2210
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-915-287

Query Match 96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

78 GGAGCGCGCCAGAGGCTCTGAGGCGGACCCGAGACCTGGCTGGCGAGATGAAGTAT 137
52 GGAGCGCGCCAGAGGCTCTGAGGCGGACCCGAGACCTGGCTGGCGAGATGAAGTAT 111
138 CTCGGGCAACGGGCGGCCAATGCACTTCATTTGGCCATCGGCGCTTTCACCTCTCTC 197
112 CTCGGGCAACGGGCGGCCAATGCACTTCATTTGGCCATCGGCGCTTTCACCTCTCTC 171
198 CTCCTGAGTCTGCTAGTGTACCACTCACTTGAAGTCCAGAGAGCAAGCCGCGATC 257
172 CTCCTGAGTCTGCTAGTGTACCACTCACTTGAAGTCCAGAGAGCAAGCCGCGATC 231
258 CCCGAGGCGCTGAGGCGGCCAATGCACTTCACCCGCGGCGGCCGCGGCGATGCG 317
232 CCCGAGGCGCTGAGGCGGCCAATGCACTTCACCCGCGGCGGCCGCGGCGATGCG 291
318 AACACCTCTATGAGTCAACCCAGCGGACTTTCGCGACGAGCGGCGAGCACTTCAAGTTC 377
292 AACACCTCTATGAGTCAACCCAGCGGACTTTCGCGACGAGCGGCGAGCACTTCAAGTTC 351
378 CTCCTGTAACAAGCTGCGGCACTTTCCTGCTGCGAGAGCGTCCCTCTTAAGTGC 437
352 CTCCTGTAACAAGCTGCGGCACTTTCCTGCTGCGAGAGCGTCCCTCTTAAGTGC 411
438 GGGAGCGGCTCTCTGCTGCTGAGTCAAGTCTCTCCCTAAGCACTAATGCGCGCG 497
412 GGGAGCGGCTCTCTGCTGCTGAGTCAAGTCTCTCCCTAAGCACTAATGCGCGCG 471
498 GAGCTGCTCGGCGCACTGAGGCGCGGAGCGCAAGTCAAGGAGTTCAGCTGCGCTC 557
472 GAGCTGCTCGGCGCACTGAGGCGCGGAGCGCAAGTCAAGGAGTTCAGCTGCGCTC 531
558 CTCCTTCTGAGTGGCAAGCTTCAACCGGCAAGAGCGCGGAGTCAACCGGCTGCTG 617
532 CTCCTTCTGAGTGGCAAGCTTCAACCGGCAAGAGCGCGGAGTCAACCGGCTGCTG 591
618 GAGCTGAGGCAAGCTCAAGGAGCACTCGGCAAGTCAAGGAGTTCAGCTGCGCTC 677
592 GAGCTGAGGCAAGCTCAAGGAGCACTCGGCAAGTCAAGGAGTTCAGCTGCGCTC 651
678 AACCTCAAGCTCAAGGAGTCTGTTCTTAAGTGGCAGAGCAAGTGGCGCAAGCGC 737
652 AACCTCAAGCTCAAGGAGTCTGTTCTTAAGTGGCAGAGCAAGTGGCGCAAGCGC 711
738 AGCTTGTGCTCAACGGGAGTGAAGTGTCTTTGCAACAACAAGATGCTTTTCAAC 797
712 AGCTTGTGCTCAACGGGAGTGAAGTGTCTTTGCAACAACAAGATGCTTTTCAAC 771

798 CTGAGAGCAATGACCTTGGCCGCACTTCTGAGGCAACTGATCAAAAAGTGGGC 857
772 CTGAGAGCAATGACCTTGGCCGCACTTCTGAGGCAACTGATCAAAAAGTGGGC 831
858 CCCATCCGGGCTTTTGGAGCAAGTATGATGCGAGAGTGGTGAATCAAGTACCGG 917
832 CCCATCCGGGCTTTTGGAGCAAGTATGATGCGAGAGTGGTGAATCAAGTACCGG 891
918 TACCACTTATTTGGGGGGGGGGCTTTCCTGCTGCTCCGCTTCAAGCGGCGCTCCG 977
892 TACCACTTATTTGGGGGGGGGGCTTTCCTGCTGCTCCGCTTCAAGCGGCGCTCCG 951
978 GCGCTGCTCCCATGCTTTCGACATCTTCCCATGATGATGCTTTCGAGATGATG 1037
952 GCGCTGCTCCCATGCTTTCGACATCTTCCCATGATGATGCTTTCGAGATGATG 1011
1038 CTGAGCTTGAAGGAGCTGAAGCTTCCCAAGCGGCGATCCGACGTTGGCGTGG 1097
1012 CTGAGCTTGAAGGAGCTGAAGCTTCCCAAGCGGCGATCCGACGTTGGCGTGG 1071
1098 GCTTCATGGCAACACCTGCTCTTGAACCCGCTCTTACGAGACCTGCTGCTGG 1157
1072 GCTTCATGGCAACACCTGCTCTTGAACCCGCTCTTACGAGACCTGCTGCTGG 1131
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1192 ACTTCGGCAATCAAGCAACAGATCTAAGATCAAGATCAAGGATCCCAAGCTTGGGCT 1251
1278 CCGTCTTCAAGAGAGGGGGGCAACTTCCCTCCAGAGAGTGAACCTTGTGCTGG 1337
1252 CCGTCTTCAAGAGAGGGGGGCAACTTCCCTCCAGAGAGTGAACCTTGTGCTGG 1311
1338 AGCATTAAGGAGTGCAGAGGAGGTTTGAAGTATGATGAATATTTGCTGCGGCA 1397
1312 AGCATTAAGGAGTGCAGAGGAGGTTTGAAGTATGATGAATATTTGCTGCGGCA 1371
1398 CTCCTACACATCTTCAAAAACCACTGGTATCTGTTCCAGATCTTCCCTGGATGGCTGG 1457
1372 CTCCTACACATCTTCAAAAACCACTGGTATCTGTTCCAGATCTTCCCTGGATGGCTGG 1431
1458 AGGAATCCAGAAATATGCACTTCTTTTGTGCTGTATATGCAAGAGCGCTGCGC 1517
1432 AGGAATCCAGAAATATGCACTTCTTTTGTGCTGTATATGCAAGAGCGCTGCGC 1491
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1492 TAGAGTCCAACTGAGATGCACTCCGCTCCGTTTGAATCAAGTCTTACTTCCGCTCT 1551
1578 CACTTAATCAAGAGGAGTGTAAAGAGTGAACCTGCAAGTGTATATGCAATAGC 1637
1552 CACTTAATCAAGAGGAGTGTAAAGAGTGAACCTGCAAGTGTATATGCAATAGC 1611
1638 TCCGCTGAGTTCAGAGCGCAAGCACTCCGCTGCTCAATGAGTGAAGTGAAG 1697
1612 TCCGCTGAGTTCAGAGCGCAAGCACTCCGCTGCTCAATGAGTGAAGTGAAG 1671
1698 ATATCTTTCAGCGCGAGAGAGGGGCTCTGATCTTAAACCTTTCCTGGGCTCAGACAA 1757
1672 ATATCTTTCAGCGCGAGAGAGGGGCTCTGATCTTAAACCTTTCCTGGGCTCAGACAA 1731
1758 CTCAAGAGTGGGGGATACCAAGAGTGTGAATAGAACCGCGCTCTCTTAACCTG 1817
1732 CTCAAGAGTGGGGGATACCAAGAGTGTGAATAGAACCGCGCTCTCTTAACCTG 1791
1818 TGGATCAAAATCTGTAATGTTGAGAGTGTGGCAGAGAGGAGCAAGTCTTTTGA 1877
1792 TGGATCAAAATCTGTAATGTTGAGAGTGTGGCAGAGAGGAGCAAGTCTTTTGA 1851

QY 1878 AGTGTGAGAGCTCAGAGTTTCTGGGGTCCCTATTAGAGAGCCCATCCCTGTGTTCCC 1937
DB 1852 AGTTGTAGAGCTCAGAGTTTCTGGGGTCCCTATTAGAGAGCCCATCCCTGTGTTCCC 1911
QY 1938 AAGATTGAGAGAACACACACTGGGGCTGGAATGATCTTTAATGGGCCCAAGCAAGG 1997
DB 1912 AAGAAATTCAGAGAACACACACTGGGGCTGGAATGATCTTTAATGGGCCCAAGCAAGG 1971
QY 1998 CATATGCTCAGTACCTGCTGGAGAGAGAGATTGAGGCTCCAGAGCCCTCCCTCA 2057
DB 1972 CATATGCTCAGTACCTGCTGGAGAGAGAGATTGAGGCTCCAGAGCCCTCCCTCA 2031
QY 2058 CCCAGTATGTTTTCAGATTACGGGGGAGCCGGGTGAGCCAGTACCCCTGACGCCCC 2117
DB 2032 CCCAGTATGTTTTCAGATTACGGGGGAGCCGGGTGAGCCAGTACCCCTGACGCCCC 2091
QY 2118 AGCTTCAGGCTCAGTGTCTGCGCAGTCAAGCTTCAGAGGCAATGTGATGGGGCAGCCTTG 2177
DB 2092 AGCTTCAGGCTCAGTGTCTGCGCAGTCAAGCTTCAGAGGCAATGTGATGGGGCAGCCTTG 2151
QY 2178 GGGAAATTAATAATTTTGTGAAGA 2200
DB 2152 GGGAAATTAATAATTTTGTGAAGA 2174

RESULT 12

US-10-176-484-287
Sequence 287, Application US/10176484
Publicatation No. US2003059876A9
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C64
CURRENT APPLICATION NUMBER: US/10/176,484
CURRENT FILING DATE: 2002-06-20
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 287
LENGTH: 2210
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-484-287

Query Match 96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 GAGAGCGCCGAGAGAGCTCTCAGGCGGAGCCGAGACCTGTGCTGGCAGAGATGAATAT 137
DB 52 GAGAGCGCCGAGAGAGCTCTCAGGCGGAGCCGAGACCTGTGCTGGCAGAGATGAATAT 111
QY 138 CTCGCGGACCGGGGGGCCCAATGCGACCTCATTTCTGGCCATCGGCGCTTTTCACTCTCTC 197
DB 112 CTCGCGGACCGGGGGGCCCAATGCGACCTCATTTCTGGCCATCGGCGCTTTTCACTCTCTC 171
QY 198 CTCCTCAGTCTGCTAGTGTACCAACCCAGCTGCAAGGTCCAGAGAGCAAGCCAGCGGAGTC 257
DB 172 CTCCTCAGTCTGCTAGTGTACCAACCCAGCTGCAAGGTCCAGAGAGCAAGCCAGCGGAGTC 231
QY 258 CCCGAGGCGCTGCGCTGGCCCACTCAACCCAGCCGCGGAGCCCGGAGCCCGTGCATGCC 317
DB 232 CCCGAGGCGCTGCGCTGGCCCACTCAACCCAGCCGCGGAGCCCGGAGCCCGTGCATGCC 291

QY 318 AACACCTCTATGCTCAACCAACCCGAGCTTGGCCACGAGCGGAGAGCTTCAAGACTTC 377
DB 292 AACACCTCTATGCTCAACCAACCCGAGCTTGGCCACGAGCGGAGAGCTTCAAGACTTC 351
QY 378 CTCCTCTGACAGACACTGCGCCCACTTTCCTCTGTGAGAGACGTGCCCCCTTAACTGC 437
DB 352 CTCCTCTGACAGACACTGCGCCCACTTTCCTCTGTGAGAGACGTGCCCCCTTAACTGC 411
QY 438 GCGGAGCGGCTCTTCTGCTGCTGCTGATCAAGTCTCTCCCTAGCAACTATGTGCGGCC 497
DB 412 GCGGAGCGGCTCTTCTGCTGCTGCTGATCAAGTCTCTCCCTAGCAACTATGTGCGGCC 471
QY 498 GAGCTGTGGGGGCAAGTGGGGGCGGAGCGGAGGTTAGGGGGTTTGGAGCTGCGCTC 557
DB 472 GAGCTGTGGGGGCAAGTGGGGGCGGAGCGGAGGTTAGGGGGTTTGGAGCTGCGCTC 531
QY 558 CTCCTCTGTGGGCAAGCTCTCCACCCGAGAGGCGGCAAGTCAACCGGCTGCTG 617
DB 532 CTCCTCTGTGGGCAAGCTCTCCACCCGAGAGGCGGCAAGTCAACCGGCTGCTG 591
QY 618 GAGCTGAGGCAAGACTCAACGAGACATCTGCACTTGGGACTTTCAGACTCTTCTTC 677
DB 592 GAGCTGAGGCAAGACTCAACGAGACATCTGCACTTGGGACTTTCAGACTCTTCTTC 651
QY 678 AACCTCAGCTCAAGCAGGCTCTGTTCTTACAGTGGAGAGACAAAGGTGGCCAAAGGC 737
DB 652 AACCTCAGCTCAAGCAGGCTCTGTTCTTACAGTGGAGAGACAAAGGTGGCCAAAGGC 711
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DB 712 AGCTTCGTGCTCAACGGGGATGATGAGTCTTTGACACACAGACAAATGCTTCTTAC 771
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QY 858 CCCATCCGGGCTTTTGGAGCAAGTACTATGTGCGAGAGGGGATCTCAAGATGAAGCG 917
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QY 918 TACCAACCTATTTGAGGGGTGAGTCTTCTGCTGCCCTTCAAGGCGGCTGCCCTG 977
DB 892 TACCAACCTATTTGAGGGGTGAGTCTTCTGCTGCCCTTCAAGGCGGCTGCCCTG 951
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QY 1098 GCTTCATCGCAACCTGCTCTCTTGAACCCCTGCTTCAACGAGACCTGCTGCTG 1157
DB 1072 GCTTCATCGCAACCTGCTCTCTTGAACCCCTGCTTCAACGAGACCTGCTGCTG 1131
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DB 1132 CACCGCTTCTTACCTTATGATGCTGCTCATGTGGAGTCCGCTGAACAGCCCACTC 1191
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DB 1192 ACCTGGGGCAATGAGACAGATCTACTGATGACATGAGGATCCCAACCTCTGGGCT 1251
QY 1278 CTGTTTTCAGAGGAGGCGGACACTTCTCTCCAGGAGCTGAGACTTGTGCTG 1337
DB 1252 CTGTTTTCAGAGGAGGCGGACACTTCTCTCCAGGAGCTGAGACTTGTGCTG 1311
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DB 1312 AGCATTAAGGAGTGCAGAGGAGGTTTGAAGTTTATGATGAATATTTCTGCTGCGGAA 1271

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QY 1458 AGGAACTCCAGAAAATATGATCTCTTTTGTGCTGTAATGGCAAGTCCGTGGC 1517
DB 1432 AGGAACTCCAGAAAATATGATCTCTTTTGTGCTGTAATGGCAAGTCCGTGGC 1491
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QY 1578 CACCTACTCAGACGCGGATGCTAGACATGCACTGCACTGCTTTAATGGCAATAGC 1637
DB 1552 CACCTACTCAGACGCGGATGCTAGACATGCACTGCACTGCTTTAATGGCAATAGC 1611
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DB 1732 CTCAGAAAGTTGGGGGATACCAAGAGGTGTGGAATAGAACCCGCCCTCCTACTTG 1791
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DB 1792 TGGGATCAAAATGCTGTAATGTGGAAGGTGTGGCAGAGAGAGGCAAGTGTCTTTGAA 1851
QY 1878 AGTTGAGAGCTCAGAGTTCTGAGGTCCTCATTAAGAACCCCACTCCTGTGTTCCC 1937
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DB 1912 AAGAAATTCAGAGAACAGACCTGGGGCTGGAATGATCTTTAATGGGCCCAAGGCCAAG 1971
QY 1998 CATATGCTCAGTCTGCTGAGAGAGAGAGATTCAGATCTTCCAGACAGCTCCTCA 2057
DB 1972 CATATGCTCAGTCTGCTGAGAGAGAGATTCAGATCTTCCAGACAGCTCCTCA 2031
QY 2058 CCCAGTATGTTTACAGATTAACGGGGGACCGGGTGGCCAGTGAACCCCGACAGCCGCC 2117
DB 2032 CCCAGTATGTTTACAGATTAACGGGGGACCGGGTGGCCAGTGAACCCCGACAGCCGCC 2091
QY 2118 AGCTTCAGGCTCAGTGTCTGCAAGCTTCAAGCTTCAAGCAATTTGTGATGGGGCAGCTTG 2177
DB 2092 AGCTTCAGGCTCAGTGTCTGCAAGCTTCAAGCTTCAAGCAATTTGTGATGGGGCAGCTTG 2151
QY 2178 GGGAAATATAAATTTTGTGAAGA 2200
DB 2152 GGGAAATATAAATTTTGTGAAGA 2174
RESULT 13
US-10-180-550-287
; Sequence 287, Application US/10180550
; Publication No. US2003006440A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C149
; CURRENT APPLICATION NUMBER: US/10/180,550
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 287
; LENGTH: 2210
; ORGANISM: Homo Sapien
; US-10-180-550-287
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Query Match 96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 78 GAGAGCCGCGCAGAGAGGCTCTCAGGCGGACCCAGACCTCGTGGCCAGAGTAAATAT 137
DB 52 GAGAGCCGCGCAGAGAGGCTCTCAGGCGGACCCAGACCTCGTGGCCAGAGTAAATAT 111
QY 138 CTCGGGACCGGCGGCCCAATGACACCTCAATCTGGCCATCGGCGCTTACCCCTCTC 197
DB 112 CTCGGGACCGGCGGCCCAATGACACCTCAATCTGGCCATCGGCGCTTACCCCTCTC 171
QY 198 CTCCTAGCTGTAGTGTCAACCAACCACTGCAAGGTCCAGAGACCCAGCGGCGATC 257
DB 172 CTCCTAGCTGTAGTGTCAACCAACCACTGCAAGGTCCAGAGACCCAGCGGCGATC 231
QY 258 CCCGAGGCCCTGGCTGGCCCACTCCACCCAGCCGCGGCGGCGGCGGCGGCGGCGGCGG 317
DB 232 CCCGAGGCCCTGGCTGGCCCACTCCACCCAGCCGCGGCGGCGGCGGCGGCGGCGGCGG 291
QY 318 AACACTCTATGATGATACCAACCCGAGCTTGCAGAGCGGCGGCGGCGGCGGCGGCGG 377
DB 292 AACACTCTATGATGATACCAACCCGAGCTTGCAGAGCGGCGGCGGCGGCGGCGGCGG 351
QY 378 CTCCTGTACAGACATGCGCGGCACTTTCCTCGCTGAGAGAGTGGCCGCTCTAAGTGC 437
DB 352 CTCCTGTACAGACATGCGCGGCACTTTCCTCGCTGAGAGAGTGGCCGCTCTAAGTGC 411
QY 438 GGGAGCGGCGGCTTCTGCTGTGTGATCAAGTCTCCCTAGCACTATGTGGCGCG 497
DB 412 GGGAGCGGCGGCTTCTGCTGTGTGATCAAGTCTCCCTAGCACTATGTGGCGCG 471
QY 498 GAGCTGCTGCGGCGACGTGGGCGCGAGCGCAAGTACCGGGTTTTCAGTGGCGCTC 557
DB 472 GAGCTGCTGCGGCGACGTGGGCGCGAGCGCAAGTACCGGGTTTTCAGTGGCGCTC 531
QY 558 CTCCTTCTGTGGGCAAGCTCTCAACCGGCGAGAGCCCGCAAGTCAACCGGCTGCTG 617
DB 532 CTCCTTCTGTGGGCAAGCTCTCAACCGGCGAGAGCCCGCAAGTCAACCGGCTGCTG 591
QY 618 GAGCTGAGGACAGACTCAGGAGACATCTGCAAGTGGGACTTCAAGTCTCTTCTTC 677
DB 592 GAGCTGAGGACAGACTCAGGAGACATCTGCAAGTGGGACTTCAAGTCTCTTCTTC 651
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DB 652 AACCTCAAGCTCAAGAGAGTCTGTCTTACAGTGGCAGAGACAGTGGCGCAAGCGC 711
QY 738 AGCTTGCTGCTCAACGGGAGTATGAGTCTTTGCAACAGACAACTGCTTCTAC 797
DB 712 AGCTTGCTGCTCAACGGGAGTATGAGTCTTTGCAACAGACAACTGCTTCTAC 771
QY 798 CTCGAGAGACCATGACCTGCGCGCACCTTCTGTGGGGCACTGATCCAAAACGTGGGC 857
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QY 858 CCCATCGGGCTTTTGGACAGTACTATGTCGCAAGAGGTGTGACTCAGATGAGCGG 917
DB 832 CCCATCGGGCTTTTGGACAGTACTATGTCGCAAGAGGTGTGACTCAGATGAGCGG 891
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Qy 978 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1037
Db 952 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
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Qy 1098 GCTTCATGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157
Db 1072 GCTTCATGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1131
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Db 1132 CACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191
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Qy 1278 CTTGTTTCAAG 1337
Db 1252 CTTGTTTCAAG 1311
Qy 1338 AGCATTAAG 1397
Db 1312 AGCATTAAG 1371
Qy 1398 CTCTTACATCTCTTCAAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1457
Db 1372 CTCTTACATCTCTTCAAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1431
Qy 1458 AGGAATCTCAAGAAATATGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1517
Db 1432 AGGAATCTCAAGAAATATGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1491
Qy 1518 TAGAGTTCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1577
Db 1492 TAGAGTTCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1551
Qy 1578 CACTTACTCAAG 1637
Db 1552 CACTTACTCAAG 1611
Qy 1638 TCCGCTGCAAGTTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1697
Db 1612 TCCGCTGCAAGTTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1671
Qy 1698 ATATCTTTCAAGCCAG 1757
Db 1672 ATATCTTTCAAGCCAG 1731
Qy 1758 CTCAAGAGAGTTGGGGGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1817
Db 1732 CTCAAGAGAGTTGGGGGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1791
Qy 1818 TGGGATCAATATGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1877
Db 1792 TGGGATCAATATGCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1851
Qy 1878 AGTTGTAAGAGCTCAAGAGTTTGGGGTCTCATTTAGAGAGAGAGAGAGAGAGAGAGAG 1937
Db 1852 AGTTGTAAGAGCTCAAGAGTTTGGGGTCTCATTTAGAGAGAGAGAGAGAGAGAGAGAG 1911
Qy 1938 AAGAAATTCAG 1997
Db 1912 AAGAAATTCAG 1971
Qy 1998 CATATGCTCACTGCTGAG 2057

Db 1972 CATATGCTCACTGCTGAG 2031
Qy 2058 CCCAGTATGTTTTCACATTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2117
Db 2032 CCCAGTATGTTTTCACATTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2091
Qy 2118 AGCTTCAAGGCTCAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2177
Db 2092 AGCTTCAAGGCTCAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2151
Qy 2178 GGGAAATATAAATTTTGTGAAGA 2200
Db 2152 GGGAAATATAAATTTTGTGAAGA 2174

RESULT 14
US-10-183-014-287
: Sequence 287, Application US/10183014
: Publication No. US2003006441A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zhenli
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OR INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C170
: CURRENT APPLICATION NUMBER: US/10/183,014
: CURRENT FILING DATE: 2002-06-26
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 287
: LENGTH: 2210
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-183-014-287

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 112 CTCGCGAGAGCGGCGGCGCAATGCGACCTGATTTGCGAGCATGCGGCTTTCAACCTCTCTC 171
Qy 198 CTCCTGAGTGTGTAAGTGTACCAACCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 257
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Qy 258 CCGGAGGCGCTGAGCTGCGGCGCACTCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 317
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Qy 318 AACACCTTATGATGATCAACCGAT 377
Db 292 AACACCTTATGATGATCAACCGAT 351
Qy 378 CTCCTGTACAGACATGCGGCGCACTTTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 437
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TYPE: DNA
ORGANISM: Homo Sapien
US-10-187-738-287

Query Match 96.1%; Score 2119.8; DB 13; Length 2210;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 112 CTCGCGACCGCGCGCCCAATGCCACCTCAATTTGCGCATCGCGCTTTCACCTCTCTC 171
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DB 172 CTCTTCAAGTCTGCTAGTGTACACCACTGCAAGGTCCAGAGCAGCCACCGCGCATC 231
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DB 232 CCCGAGGCCCTGGCGCTGGCCCACTCAACCAACCGCCGACCGCGCGCGCTGCGCATGCC 291
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DB 412 GCGCAGCCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
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QY 1638 TCCGTGTGAGTTCAGAGCGCGCAAGAACTCTGTGTCCACTAATGAGTGTGAGTGA 1697
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QY 1998 CATATGCTTCACTACTGCTGTGAGAGGAGAGATTCAGGTCTTCCAGCAGCTCTCTCA 2057
DB 1972 CATATGCTTCACTACTGCTGTGAGAGGAGAGATTCAGGTCTTCCAGCAGCTCTCTCA 2031
QY 2058 CCAAGTATGTTTATCAAGATTTACGGGGGAGACCGGGTGAAGCAGTGAACCTCTGAGCCCTC 2117
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Search completed: June 14, 2004, 17:03:40
Job time : 1796 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2004, 10:06:10 ; Search time 5670 Seconds

(without alignments)
11613.070 Million cell updates/sec

Title: US-10-019-735-6

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	883.6	40.1	914	9	AL555347
C 2	882.6	40.0	951	13	AL555347 BX386504
C 3	856.8	38.9	957	13	BX386505 BX386505
C 4	822.8	37.3	878	13	BX350525 BX350525

Result No.	Score	Query Match	Length	ID	Description
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6	795.6	36.1	889	9	AL555348
7	787	35.7	840	13	BX387833
8	766.4	34.8	878	13	BX387834
9	763.2	34.6	1201	13	BX387834
10	751.2	34.1	1201	9	AL552030
11	701.8	31.8	808	14	CD559737
12	694.2	31.5	1201	9	AL551994
13	691.4	31.4	720	12	BM682980
14	666.4	30.2	680	12	BM718996
15	633.4	28.7	808	14	CD559581
16	623.4	28.3	655	12	BM976865
17	618.2	28.0	821	14	CD559582
18	591.4	26.8	1155	13	BX359759
19	572.2	26.0	1963	11	AK008674
20	544	24.7	589	9	AL709364
21	537.8	24.4	542	9	AL699036
22	513	23.3	585	12	BM837166
23	511.2	23.2	540	9	AM083360
24	489	22.2	491	10	BF435128
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28	464.2	21.1	611	13	BQ366411
29	462.4	21.0	476	10	BE644881
30	457.4	20.7	470	9	AA552613
31	455.8	20.7	480	9	AM610408
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33	452.2	20.5	480	12	BS980262
34	449.8	20.4	466	9	AL738745
35	443.4	20.1	461	9	AL684023
36	438	19.9	496	12	BM751524
37	432	19.6	432	13	EX483385
38	431.2	19.6	451	10	AM610431
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ALIGNMENTS

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DEFINITION AL555347 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CSODK008Y002 3-PRIME, mRNA sequence.
ACCESSION AL555347
VERSION AL555347.2 GI:31277155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 914)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12896993.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9600.f For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODK008Y002INP1&cluster=9600.f. Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK008BH01NP1.
 Location/Qualifiers

FEATURES

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

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Query Match      40.1%; Score 883.6; DB 9; Length 914;
Best Local Similarity 97.7%; Pred. No. 1.7e-180;
Matches 892; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

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1803  CCCCCTCTTAATTTGGAGTCAATGCTGTAATGAGTGGAGTGGAGGAGGAG 1862
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1863  GCAAGTCTTTGAAAGTTGAGAGCTCAAGATTTCTGGGGTCTCTATGAGAGCC 1922
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DEFINITION BX386504 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX386504
VERSION BX386504.1 GI:30436819
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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REFERENCE 1 (bases 1 to 951)
AUTHORS Li W.B., Gruber C., Jessee J. and Polayres D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9600.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AI022D05NP1&cluster=9600.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AI022D05NP1.
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FEATURES

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

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Query Match      40.0%; Score 882.6; DB 13; Length 951;
Best Local Similarity 97.8%; Pred. No. 2.8e-180;
Matches 915; Conservative 7; Mismatches 11; Indels 3; Gaps 3;

1235  ACAGATCTACTAGTACATCAGAGGT-CCCAAGCTCTGGAGTCTGTTTCCAGAGAA 1293
951  ACAKRTTACTGAGTACAGATMAGAGGTCCCAAGCTCTGGAGTCTGTTTCCAGT- 993
1294  GGGGCGACACCTTCCCAAGAAAGTGAAGCTTTGTGTGCTGACATTAAGGAATGCC 1353
892  GGGGCGACACCTTCCCAAGAAAGTGAAGCTTTGTGTGCTGACATTAAGGAATGCC 833
1354  AGGAAGTTTGAAGTTTGAAGTGAATATTCTGCTGGCGAATCCTTACATCCTTC 1413
832  AGGAAGTTTGAAGTTTGAAGTGAATATTCTGCTGGCGAATCCTTACATCCTTC 773
1414  AAAAACCACCTGTAAGTCTTCCAGATCTTCCCTGAGTGGCTGAGAACTCCAGAAAT 1473
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 Qy 1714 GAGAGAGGGGTCTGATCTTAACTCTTCTGGGTCTCAGACACTCAGAAAGTTGGGG 1773
 Db 472 GAGAGAGGGGTCTGATCTTAACTCTTCTGGGTCTCAGACACTCAGAAAGTTGGGG 413
 Qy 1774 GATACCAAGAGAGTGTGGAATAGACCGCCCTCTCTTACTTGTGGATCAAAATGCTGT 1833
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 Qy 1834 AATGTGAGAGTGTGTGGCAGAGAGAGAGAGAGAGTGT-CTTGAAGTTGTGAGCTCA 1892
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 ACCESSION Bx386505
 VERSION Bx386505.1 GI:30440702
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 957)
 REFERENCES
 1. W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 9600.f for

more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS1A10222D050Pl&cluster=9600.f)
 seqref@genoscope.cns.fr
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600ParadeyAvenueGenoscopeSequenceID:CS1A10222D050Pl>.

FEATURES
 source
 1..957
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="RNA"
 /db_xref="taxon:9606"
 /clone="CS0D1086YB09"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="First strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 38 9%; Score 856.8; DB 13; Length 957;
 Best Local Similarity 98.3%; Pred. No. 1.1e-174; Indels 3; Gaps 3;
 Matches 891; Conservative 5; Mismatches 7;

163 CCTCATCTGCGCAGTCGCGGCTTTCACCTCTCTCTTCACTGCTAGTGCACAC 222
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 47 CCGGAATTCGCGGATCGGCGCTTTCACCTCTCTCTTCACTGCTAGTGCACAC 106
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 223 CCACCTGCAGAGTCCAGAGCAGCAGCGCGATCCCGAGGCGCTGCGCCCACTC 282
 |||||
 107 CCACCTGCAGAGTCCAGAGCAGCAGCGCGATCCCGAGGCGCTGCGCCCACTC 165
 |||||
 283 CACCCACCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 342
 |||||
 166 CACCCACCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 225
 |||||
 343 ACTTGCCACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 402
 |||||
 226 ACTTGCCACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 285
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 403 TTCCCTGCTGAGAGCGTCCCTCTTAACTGCGCGAGCGAGCGAGCGAGCGAG 462
 |||||
 286 TTCCCTGCTGAGAGCGTCCCTCTTAACTGCGCGAGCGAGCGAGCGAGCGAG 344
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 463 TGATCAAGTCTCTCTCTTCACTATGTCGCGCGAGCGAGCGAGCGAGCGAG 522
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 345 TGATCAAGTCTCTCTCTTCACTATGTCGCGCGAGCGAGCGAGCGAGCGAG 404
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 523 GCGAGCGAGGTAAGGAGTTTGAAGTGCAGCTGCGCTCTCTTCTGAGGAGCA 582
 |||||
 405 GCGAGCGAGGTAAGGAGTTTGAAGTGCAGCTGCGCTCTCTTCTGAGGAGCA 464
 |||||
 583 ACCCGCAGAGGCGCGCAGAGTCAACCGGCTGCTGAGAGTGAAGCAGACTCAG 642
 |||||
 465 ACCCGCAGAGGCGCGCAGAGTCAACCGGCTGCTGAGAGTGAAGCAGACTCAG 524
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 643 ACATCTGCAAGTGGAGTCTTCAAGTCTCTTCACTCACTCAAGTCAAGTCAAG 702
 |||||
 525 ACATCTGCAAGTGGAGTCTTCAAGTCTCTTCACTCACTCAAGTCAAGTCAAG 584
 |||||
 703 TCTTACAGTGGCAGAGCAAGGAGTGCAGCAGCAGCTTCTGAGTCAAGCAGGATGAT 761
 |||||
 585 TCTTACAGTGGCAGAGCAAGGAGTGCAGCAGCAGCTTCTGAGTCAAGCAGGATGAT 644
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 762 GACGCTTTTGCACACACAGACAACTGCTTCTTCACTGACAGACATGACCTGCGCG 821
 |||||
 645 GACGCTTTTGCACACACAGACAACTGCTTCTTCACTGACAGACATGACCTGCGCG 704
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 822 CACCTCTTGTGGGGCACTGATCCAAAGTGGGGCCCTTCCGGCTTTTGGAGCAG 881
 |||||
 705 CACCTCTTGTGGGGCACTGATCCAAAGTGGGGCCCTTCCGGCTTTTGGAGCAG 764
 |||||
 882 TACTATGTGCCAGAGTGTGATCTCAGATGAGCGGTACCCACCTATTTGAGGATGAT 941

Db 765 TACTATGTCAGAGAGTGTGATCTCAAGATAGAGCGTATCCACCTTATTGAGGGTGTGT 824
Qy 942 GCGTCTTGCTGTCTCCCGCTTCAAGCGCCGCTGCGCCCTGCGCCGCTGCTGAGCTTCTTGAGC 1001
Db 825 GCGTCTTGCTGTCTCCCGCTTCAAGCGCCGCTGCGCCCTGCGCCGCTGCTGAGCTTCTTGAGC 884
Qy 1002 ATCTTCCCATTTGATGATGTCTTCTGGGTATGTGTCTGAGCTTGAAGGACTGAAGCT 1061
Db 885 ATCTTCCCATTTGATGATGTCTTCTGGGTATGTGTCTGAGCTTGAAGGACTGAAGCT 944
Qy 1062 GCGTCC 1067
Db 945 GCGTCC 950

RESULT 4
BX350525/c 878 bp mRNA linear EST 05-MAY-2003
LOCUS BX350525 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK008Y002 3-PRIME, mRNA sequence.
ACCESSION BX350525
VERSION BX350525.1 GI:30383512
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9600.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BA10392E05_CS03685_1&cluster=9600.f.
Contact : Feng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0BA10392E05_CS03685_1.
location/Qualifiers
1. 878
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK008Y002"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_1ib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 37.3%; Score 822.8; DB 13; length 878;
Best Local Similarity 98.4%; Pred. No. 2.5e-167;
Matches 841; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Db 636 CACGAGACATCTGTGAGTGGAGCTTCAAGACTCTTCTTCAACCTCAAGCTCAAGAG 695
Qy 576 GCGTCCAAACCGGACGAGCGCCGCAAGCTCAACCGGCTCTGAGCTGAGGCAAGACT 635
Db 817 GCGTCCAAACCGGACGAGCGCCGCAAGCTCAACCGGCTCTGAGCTGAGGCAAGACT 758
Qy 636 CACGAGACATCTGTGAGTGGAGCTTCAAGACTCTTCTTCAACCTCAAGCTCAAGAG 695

Db 757 CACGAGACATCTGTGAGTGGAGCTTCAAGACTCTTCTTCAACCTCAAGCTCAAGAG 698
Qy 696 GTCTCTTTCTTACAGTGCAGAGAGACAAAGGTGGCCCAACCGACCTTCGTCTCAAGGG 755
Db 697 GTCTCTTTCTTACAGTGCAGAGAGACAAAGGTGGCCCAACCGACCTTCGTCTCAAGGG 638
Qy 756 GATGATGACGTCTTTGACACACAGACAAACATGTCTTTCTTCACTGACAGACATGACCT 815
Db 637 GATGATGACGTCTTTGACACACAGACAAACATGTCTTTCTTCACTGACAGACATGACCT 578
Qy 816 GCGCGCCACCTCTTGTGGGGCAACGTATCCAAAACGTGGGCCCATTCGGGCTTTTGG 875
Db 577 GCGCGCCACCTCTTGTGGGGCAACGTATCCAAAACGTGGGCCCATTCGGGCTTTTGG 518
Qy 876 AGCAAGTACTATGTGCCAGAGGTGTGACTGAAATAGAGGGGTATCCACCTATTGTTGG 935
Db 517 AGCAAGTACTATGTGCCAGAGGTGTGACTGAAATAGAGGGGTATCCACCTATTGTTGG 458
Qy 936 GGTGTGGCTCTTGTGCTGTCCCGCTTCAAGCGCCGCTGCGCCGCTGCTGAGCTTGCATGTC 995
Db 457 GGTGTGGCTCTTGTGCTGTCCCGCTTCAAGCGCCGCTGCGCCGCTGCTGAGCTTGCATGTC 398
Qy 996 TTGACATCTTCCCATTTGATGATGTCTTCTGGGTATGTGTCTGAGCTTGAAGGACTG 1055
Db 397 TTGACATCTTCCCATTTGATGATGTCTTCTGGGTATGTGTCTGAGCTTGAAGGACTG 338
Qy 1056 AAGCTGCTGCCACAGCGGATCCGACGCTGCGGGGCTCCATCGCAACACCTG 1115
Db 337 AAGCTGCTGCCACAGCGGATCCGACGCTGCGGGGCTCCATCGCAACACCTG 278
Qy 1116 TCTCTCTTGAACCCCTGCTTACCGAGACCTGTGCTGTGACACCGCTTCTTACTTAT 1175
Db 277 TCTCTCTTGAACCCCTGCTTACCGAGACCTGTGCTGTGACACCGCTTCTTACTTAT 218
Qy 1176 GAGATGCTGCTCAATGTGGAGATGCGCTGAACCAACCACTTCACTGTGGAGATGAGCA 1235
Db 217 GAGATGCTGCTCAATGTGGAGATGCGCTGAACCAACCACTTCACTGTGGAGATGAGCA 158
Qy 1236 CAGATCTACTAGTCAGATGAGGATCCGACGCTGTGGGCTCTGTTTCCAGAGGAG 1295
Db 157 CAGATCTACTAGTCAGATGAGGATCCGACGCTGTGGGCTCTGTTTCCATGAGAGG 98
Qy 1296 GCGGACACCTTCTTCCAGAGGAGTGAACCTTTGTGTCTGAGCATTAAGGAGTGCAG 1355
Db 97 GCGGACACCTTCTTCCAGAGGAGTGAACCTTTGTGTCTGAGCATTAAGGAGTGCAG 38
Qy 1356 GGAGCTTTGAGGTT 1370
Db 37 GGAGCTTTGAGGTT 23

RESULT 5
BX390709 950 bp mRNA linear EST 13-MAY-2003
LOCUS BX390709 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK008Y002 5-PRIME, mRNA sequence.
ACCESSION BX390709
VERSION BX390709.1 GI:30619197
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 950)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9600.f For

more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BA0462B12_CS04410_1&cluster=9600.f.
 Contact : Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0BA0462B12_CS04410_1.
 Location/Qualifiers

FEATURES
 source

1. 950
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK008Y002"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_1lb="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 36.1%; Score 796.8; DB 13; Length 950;
 Best Local Similarity 94.0%; Pred. No. 1.1e-161;
 Matches 893; Conservative 0; Mismatches 49; Indels 8; Gaps 6;

QY 730 CCAAGCGCAGCTTCGCTCAACGGGGATGATGACCTTTGGACACAGACAAATG- 788
 DB 2 CAAGCGCAGCTTCGCTCAACGGGGATGATGACCTTTGGACACAGACAAATG- 61
 QY 789 GTCTTCTACCTGACGAGACCATGACCTCGGCGCCGACCTTCGTGGGGCAACTGATCA- 848
 DB 62 GTCTTCTACCTGACGAGACCATGACCTCGGCGCCGACCTTCGTGGGGCAACTGATCA- 121
 QY 849 AACGTGGCGCCCAATCCGGGCTTTTGGAGCAAGTACTATGTGCGAGAGGTGTACTGAG- 908
 DB 122 AACGTGGCGCCCAATCCGGGCTTTTGGAGCAAGTACTATGTGCGAGAGGTGTACTGAG- 181
 QY 909 AATGAGCGGTAACCAACCTATGTGGGGGTGTGGTCTTGTGTCGCCGCTTACAGGCG- 968
 DB 182 AATGAGCGGTAACCAACCTATGTGGGGGTGTGGTCTTGTGTCGCCGCTTACAGGCG- 241
 QY 969 GCTGCGCTGCGCGGCTGCTCCCATGCTTGGACATCTTCCCATGATGATGCTTCTG- 1028
 DB 242 GCTGCGCTGCGCGGCTGCTCCCATGCTTGGACATCTTCCCATGATGATGCTTCTG- 301
 QY 1029 GGTATGTGCTGAGAGCTTGAAGGACCTGCTCCCAAGCGGCAATCCGACGTCT- 1088
 DB 302 GGTATGTGCTGAGAGCTTGAAGGACCTGCTCCCAAGCGGCAATCCGACGTCT- 361
 QY 1089 GCGCGTGGCGGCTTCATCCGAAACCTGTCTCTTGAACCCCTGCTTTCACGAGACTG- 1148
 DB 362 GCGCGTGGCGGCTTCATCCGAAACCTGTCTCTTGAACCCCTGCTTTCACGAGACTG- 421
 QY 1149 CTGCTGAGTACACGCTTCTTACCTTATGAGATGCTGCTCATGAGGATGCGCTGAAC- 1208
 DB 422 CTGCTGAGTACACGCTTCTTACCTTATGAGATGCTGCTCATGAGGATGCGCTGAAC- 481
 QY 1209 CCAACCTGACCTGGCGCAATCAGACAGATCTACTGAGTCAAGCATCGGTCGCCAC- 1268
 DB 482 CCAACCTGACCTGGCGCAATCAGACAGATCTACTGAGTCAAGCATCGGTCGCCAC- 541
 QY 1269 CTCTGGGCTCTCTGTTTCCAGAGAGAGGCGGCACTTCTCTCCAGAGAGCTGAGACTT- 1328
 DB 542 CTCTGGGCTCTCTGTTTCCAGAGAGAGGCGGCACTTCTCTCCAGAGAGCTGAGACTT- 601
 QY 1329 TGTGCTGAGCATTAAGAGAGTGCAGGAGAGTTTGAAGTTTGAATGATTAATTCTG- 1388
 DB 602 TGTGCTGAGCATTAAGAGAGTGCAGGAGAGTTTGAAGTTTGAATGATTAATTCTG- 661
 QY 1389 GCTGGGAACTCTTACATCTTCAAAACCACTGTGATCTGTTCCAGACTC-TTCCCT- 1447
 DB 662 GCTGGGAACTCTTACATCTTCAAAACCACTGTGATCTGTTCCAGACTC-TTCCCT- 721

QY 1448 GGATGGC-TGAGAGAACTCCAGAAAATATGATC-TCCTTTTGTGGCTGATATGGCA- 1504
 DB 722 GATGAGCTTGAAGAGATCCAGAAAATATCATTCTTTTGTGGCTGATATGGCA- 781
 QY 1505 GAAGTGC-CCTGTGCTAGAGTTTCAACTGTGATGATCGGTCGCTTTGAGTCAAGTCT- 1563
 DB 782 GAAGGCGCTGTGCTAGAGTTTCAACTGTGATGATCGGTCGCTTTGAGTCAAGTCT- 841
 QY 1564 TACTTCCCTGCTCTCACTTACACAGAGGAGTGTATAGACATGACCTGCACTGCTT- 1623
 DB 842 TATTTCCTTCTCTCT--CCTTATTAACAGAGGAGTGTGTCAGGGGCACTTGGCAGGGGTTT- 899
 QY 1624 AATGAGATTAAGTCTCCGCTGAGTTCAGGCGGCGGAGAACTGCTG- 1673
 DB 900 AATGAGATTAAGTCTCCGCTGAGTTCAGGCGGCGGAGAACTGCTG- 949

RESULT 6
 AL555348 889 bp mRNA linear EST 31-MAY-2003
 LOCUS DEFINITION
 AL555348 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 CDNA clone CS0DK008Y002 5-PRIME, mRNA sequence.
 AL555348
 AL555348.2 GI:31277156
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 889)
 Li W.B., Gruber C., Jessee J. and Polayes D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12896995.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK008BH010P1&cluster=9600.f>. Contact :
 Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK008BH010P1.
 Location/Qualifiers

FEATURES

source

1. 889
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK008Y002"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_1lb="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 36.1%; Score 795.6; DB 9; Length 889;
 Best Local Similarity 98.8%; Pred. No. 1.9e-161;
 Matches 826; Conservative 6; Mismatches 1; Indels 3; Gaps 3;

QY 44 GGAAGCTCATTTCCCTAGACGCGGCGCAAGCAAGAGCGCGCCAGAGAGCTCTCAGGC- 103
 DB 56 GGAAGCTCATTTCCCTAGACGCGGCGCAAGCAAGAGCGCGCCAGAGAGCTCTCAGGC- 115
 QY 104 GCAACCCAGAACCTTGGCTGGCCAGAGATGAATCTCCGACCGCGGCGCCCAATGCCAC- 163
 DB 116 CCAACCCAGAACCTTGGCTGGCCAGAGATGAATCTCCGACCGCGGCGCCCAATGCCAC- 175

164 CCTGATTTCTGGCAATCGGCGCTTTCACCCCTCTCTCTTCACTGCTGTAATGTCACACC 223
 176 CCTGATTTCTGGCAATCGGCGCTTTCACCCCTCTCTCTTCACTGCTGTAATGTCACACC 235
 224 CACCTGCAAGGTCCAGAGACGCCACCGGCGCA-TCCCCGAGCCCTTGCCGCTCCATC 282
 236 CACCTGCAAGGTCCAGAGACGCCACCGGCGCAATCCCGAGCCCTTGCCGCTCCATC 295
 283 CACCCACCCGCGCCAGCCCGGCGCGGCGCGCAACCTATGCTGTCACCCACCGG 342
 296 YDYACACCCGCGCCAGCCCGGCGCGGCGCGCATGCGCAACCTATGCTGTCACCCACCGG 355
 343 ACTTGGCCACGAGCGGAGCAGCACTTCAAACTTCTCTGTAAGACACATGCGGCACT 402
 356 ACTTGGCCACGAGCGGAGCAGCACTTCAAACTTCTCTGTAAGACACATGCGGCACT 415
 403 TTCCCTGCTGCAAGAGCTGCCCCCTCTTAAGTGGCGGCAAGCCGCTCTTCCGCTGCG 462
 416 TTCCCTGCTGCAAGAGCTGCCCCCTCTTAAGTGGCGGCA-SCGGTCTTCTGCTGCTGG 474
 463 TGAATCAAGTCTCCCTTACCACTAATGTCGCGGAGCTGCTGCGGCGCACTGCGGCGC 522
 475 TGAATCAAGTCTCCCTTACCACTAATGTCGCGGAGCTGCTGCGGCGCACTGCGGCGC 534
 523 GCGAGCGCAAGGTACCGGGGTTTGGAGCTGCGCTCTCTTCTGCTGCGGCAAGCTCCA 582
 535 GCGAGCGCAAGGTACCGGGGTTTGGAGCTGCGCTCTCTTCTGCTGCGGCAAGCTCCA 594
 583 ACCCGGACAGAGCGCGGCAAGGTCAACCGGCTGCTGAGCTGAGGACAGACTCAAGAG 642
 595 ACCCGGACAGAGCGCGGCAAGGTCAACCGGCTGCTGAGGAGGACAGACTCAAGAGAG 654
 643 ACATCTGCAAGTGGGAACTTTCACGACTCTTCTTCAACTCAAGCTCAAGAGAGTCTCT 702
 655 ACATCTGCAAGTGGGAACTTTCACGACTCTTCTTCAACTCAAGCTCAAGAGAGTCTCT 714
 703 TCTTACAGTGGGAGGAGCAAGGTGGCGGCAAGCGCAAGTCTGCTCAAGCGGAGATGATG 762
 715 TCTTACAGTGGGAGGAGCAAGGTGGCGGCAAGCGCAAGTCTGCTCAAGCGGAGATGATG 774
 763 ACCTCTTGGCAACAGCAACATGCTCTTCTTCAACTGACAGACATGACCTTGCGCGCC 822
 775 ACCTCTTGGCAACAGCAACATGCTCTTCTTCAACTGACAGACATGACCTTGCGCGCC 834
 823 ACCTCTTGGGAGGAGCACTGATCCAAACGTTGGGCGCCATCGGGGCTTTTGGAGC 878
 835 ACCTCTTGGGAGGAGCACTGATCCAAACGTTGGG-CCATCGCGGCTTTTGGAGC 889

RESULT 7
 BX387833/c 840 bp mRNA linear EST 08-MAY-2003
 LOCUS BX387833 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1086YB09 3-PRIME, mRNA sequence.
 ACCESSION BX387833
 VERSION BX387833.1 GI:30461784
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 9600.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0A1086CA05NP1&cluster=9600.f. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0A1086CA05NP1.
 Location/Qualifiers
 1..840
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1086YB09"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 35.7%; Score 787; DB 13; Length 840;
 Best Local Similarity 97.6%; Pred. No. 1.4e-159; Indels 3; Gaps 3;
 Matches 820; Conservative 8; Mismatches 9;

1334 TCTGAGCATTAAGGAGGAGCCAGGAGGTTGAGTTGATGATGATATTTCTGCTGG 1393
 840 TCTGAGCATTAAGGAGGAGCCAGGAGGTTGAGTTGATGATGATATTTCTGCTGG 781
 1394 GGAATCTCTACACATCTTCAAAACCCACTGCTGCTTTCAGCACTTTCC-TCGATG 1452
 780 CGGACTCTTACACATCTTCAAAACCCACTGCTGCTTTCAGCACTTTCCCTCTGATG 721
 1453 GCTGAGGAATCTCAAGAAATATGCAATCTTTTGTGCTGCTATATGAGCAAGATGCG 1512
 720 GCTGAGGAATCTCAAGAAATATGCAATCTTTTGTGCTGCTATATGAGCAAGATGCG 661
 1513 TGTGCTGAGTTTCAACTGTGATGATCCGTCCTGCTTGTGATGATG-TCCTACTTCCC 1571
 660 TGTGCTGAGTTTCAACTGTGATGATCCGTCCTGCTTGTGATGATGATGATCTTCCC 601
 1572 TGTCTCTCACTTCAAGAGCGGATGCTATGAGAGTCACTGAGAGGTTTATGAGCAG 1631
 600 TGTCTCTCACTTCAAGAGCGGATGCTATGAGAGTCACTGAGAGGTTTATGAGCAG 541
 1632 ATAGCTCCGCTGCTGAGTCCAGGCGCAGAGCAAACTCTGTGTCAATAGAGCTGACG 1691
 540 ATAGCTCCGCTGCTGAGTCCAGGCGCAGAGCAAACTCTGTGTCAATAGAGCTGACG 481
 1692 TGAGAAATATCTTTCAAGCCAGAGAGAGGAGGCTCTGATCTTAACTCTTCTGCTGCTC 1751
 480 TGAGAAATATCTTTCAAGCCAGAGAGAGGAGGCTCTGATCTTAACTCTTCTGCTGCTC 421
 1752 AGACAATCTCAAGAGGTTGGGGGATACAGAGAGGAGGATGAGACCGCCCTCTCT 1811
 420 AGACAATCTCAAGAGGTTGGGGGATACAGAGAGGAGGATGAGACCGCCCTCTCT 361
 1812 TACTTGGGATCAATGCTGTAATGTGAGGTGGGCGAGAGAGGAGGCAAGTGT- 1870
 360 TACTTGGGATCAATGCTGTAATGTGAGGTGGGCGAGAGAGGAGGCAAGTGTGTC 301
 1871 CTTTGAAGTTGTGAGAGTCAAGATTTCTGGGGCTCATTAAGAGGCCCATCTCTGT 1930
 300 CTTTGAAGTTGTGAGAGTCAAGATTTCTGGGGCTCATTAAGAGGCCCATCTCTGT 241
 1931 GTTCCCAAGATTCAGAGACAGCAGCTGGGCTGAAATGATCTTAAATGGGCCCAAGC 1990
 240 GTTCCCAAGATTCAGAGACAGCAGCTGGGCTGAAATGATCTTAAATGGGCCCAAGC 181
 1991 CAACAGCATATGCTCTCACTGCTGAGAGAGGAGAGATTCAGAGCTCTTCAAGCAGC 2050
 180 CAACAGCATATGCTCTCACTGCTGAGAGAGGAGAGATTCAGAGCTCTTCAAGCAGC 121
 2051 TCCCTCAACCAATGTTTAAAGATTAAGAGGAGGAGCGGAGTGAACAGTGAACCCCTGC 2110
 120 TCCCTCAACCAATGTTTAAAGATTAAGAGGAGGAGCGGAGTGAACAGTGAACCCCTGC 61

QY 2111 AGCCCCAGCTTCAGGCTCAGTGTCTGCGACGCTTACAGCATTTGTGATGGGCG 2170
DB 60 AGCCCCAGCTTCAGGCTCAGTGTCTGCGACGCTTACAGCATTTGTGATGGGCG 1
RESULT 8
BX387834 878 bp mRNA linear EST 08-MAY-2003
LOCUS BX387834 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION BX387834 Clone CS0D1086YB09 5-PRIME, mRNA sequence.
ACCESSION BX387834
VERSION BX387834.1 GI:30461785
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li W.B., Gruber C., Jessee J. and Polyes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9600.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1086CA05QPl&cluster=9600.f. Contact :
Feng Liang Email: fliang@life.techn.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0A1086CA05QPl.
Location/Qualifiers
1. 878
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086YB09"
/library_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 34.8%; Score 766.4; DB 13; Length 878;
Beet Local Similarity 98.0%; Pred. No. 4.1e-155;
Matches 827; Conservative 2; Mismatches 9; Indels 6; Gaps 5;
QY 163 CCTCATTTGCGCATCGCGCTTTGACCTCTCTCTTCACTGTGATGTACACAC 222
DB 37 CCGGAATTCGGGAGTCGGCGCTTACCTCTCTCTTCACTGTGATGTACACAC 96
QY 223 CCACTGCAAGTTCAGAGCAACCGGCGA-TCGCCGAGGCTTGGCTTGGCCCACT 281
DB 97 CCACTGCAAA-GTCCGAGAGCAACCGGCGA-TTCCGAGGCTTGGCTTGGCCCACT 155
QY 282 CCAACCGAGCG 341
DB 156 CCG 215
QY 342 GACTTCGACGAGCGCGAGCACTTCAAACTTCTCTCTTCACTGTGATGTACACAC 401
DB 216 GACTTCGACGAGCGCGAGCACTTCAAACTTCTCTCTTCACTGTGATGTACACAC 275
QY 402 TTTCCCTCTCTGACGAGCGTCCCTCTCTTCACTGTGATGTGCGGAGCGGTCTTCTGCTG 461
DB 276 TTTCCCTCTCTGACGAGCGTCCCTCTCTTCACTGTGATGTGCGGAGCGGTCTTCTGCTG 334
QY 462 GTGATCAAGTCTCTCCCTAGCAACTATGTGCGCGGAGCGTGTGCGGCGCACTGTGGGCG 521

DB 335 GTGATCAAGTCTCTCCCTAGCAACTATGTGCGCGGAGCGTGTGCGGCGCACTGTGGGCG 394
QY 522 CCGGAGCGCAAGGTACGGGCTTTCAGCTGCGCTCTCTCTCTTCTGTTGGGACAGCTTCC 561
DB 395 CCGGAGCGCAAGGTACGGGCTTTCAGCTGCGCTCTCTCTCTTCTGTTGGGACAGCTTCC 454
QY 582 AACCGGCAAGGCGCGCAAGGTACGGGCTTTCAGCTGCGCTCTCTCTTCTGTTGGGACAGCTTCC 641
DB 455 AACCGGCAAGGCGCGCAAGGTACGGGCTTTCAGCTGCGCTCTCTCTTCTGTTGGGACAGCTTCC 514
QY 642 GACTTCGACGAGCGCGAGCACTTCAAACTTCTCTTCACTGTGATGTGCGGAGCGGTCTTCTGCTG 701
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QY 822 CACTCTTGTGGGCGCACTGATCCAAAGTGGCGCCCATCGGCTTTTGGAGCAAG 881
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DB 875 GACA 878
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BX361506 1201 bp mRNA linear EST 05-MAY-2003
LOCUS BX361506 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION BX361506 Clone CS0D1086YB09 5-PRIME, mRNA sequence.
ACCESSION BX361506
VERSION BX361506.1 GI:30376537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li W.B., Gruber C., Jessee J. and Polyes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9600.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1086CA05QPl&cluster=9600.f. Contact :
Feng Liang Email: fliang@life.techn.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue Genoscope sequence ID : CS0D1086CA05QPl.
Location/Qualifiers
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/clone="CSOD1086YB09"
 /tissue="PLACENTA COT 25-NORMALIZED"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 34.6%; Score 763.2; DB 13; Length 1201;
 Best Local Similarity 92.5%; Pred. No. 2.4e-154;
 Matches 809; Conservative 36; Mismatches 25; Indels 5; Gaps 5;

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QY 163 CCCATTCTGGCCGCGGCTTCCACCTCTCTCTGAGTGTGAGTGTGACAC 222
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DB 112 CCACCTGCAAGTCCAGAGAGCAGCAGCCGCGATCCCGAGGCCCTGGCTGGCCACTC 171
QY 283 CACCCACCCGCCAGCCCGCGCGCTGTCATGCAACACTCTATGCTACCCACCGG 342
DB 172 CRSCACCCGCMWAGCMCGCGCGCGCTGTCATGCAACACTCTATGCTACCCACCGG 231
QY 343 ACTTGCCACGCGAGCGGAGAGCTTGAATCTCTCTGTAAGACAGACAGTCCGCACT 402
DB 222 ACTTGCCACGCGAGCGGAGAGCTTGAATCTCTCTGTAAGACAGACAGTCCGCACT 291
QY 403 TTCCCTGTCGAGAGCGTCCCGCTCTAAGTGGCGGAGCGCGTCTTCTGCTGCTG 462
DB 292 TTCCCTGTCGAGAGCGTCCCGCTCTAAGTGGCGGAGCGCGTCTTCTGCTGCTG 350
QY 463 TGATCAAGTCTCTCTTACCACTATGTCGCGCGGAGTGTGCGGCGAGAGTGGG 522
DB 351 TGATCAAGTCTCTCTTACCACTATGTCGCGCGGAGTGTGCGGCGAGAGTGGG 410
QY 523 GCGAGCGGAGGTAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 582
DB 411 GCGAGCGGAGGTAAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 470
QY 583 ACCCGCAGAGGCGCGCAAGTCAACCGGCTCTGAGAGTGGAGGCAAGTCAAGAG 642
DB 471 ACCCGCAGAGGCGCGCAAGTCAACCGGCTCTGAGAGTGGAGGCAAGTCAAGAG 530
QY 643 ACATCTGAGAGTGGAGTCTTCAAGTCTTCTTCAAGTCTTCAAGTCTTCAAGT 702
DB 531 ACATCTGAGAGTGGAGTCTTCAAGTCTTCTTCAAGTCTTCAAGTCTTCAAGT 590
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QY 883 ACTATGTGCAAGGAGTGTGATCAGATGAGCGGTAACCACTTATGAGGAGTGG 942
DB 771 GCTATGTGCAAGGAGTGTGATCAGATGAGCGGTAACCACTTATGAGGAGTGG 829
QY 943 GCTTCTGTGTCCGCTTACGCGCGTCTTGGCGGCTGCTGCTGCTGCTGCTG 1002
DB 830 GCTTCTGTGTCCGCTTACGCGCGTCTTGGCGGCTGCTGCTGCTGCTGCTG 887
QY 1003 TCTTCCCATGTATGATGCTCTTCTGAGTATGCT 1037
DB 888 TTTT-CCCATGTATGATGCTCTTCTGAGTATGCTT 921

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RESULT 10

AL552030

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AL552030 1201 bp mRNA linear EST 31-MAY-2003
 AL552030 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CSOD1060YF21 5-PRIME, mRNA sequence.
 AL552030
 AL552030.2 GI:31273846
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:12890538.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 9600.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSOD1060C110P1&cluster=9600.f. Contact :
 Feng Liang Email : fliang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
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 Location/Qualifiers
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 34.1%; Score 751.2; DB 9; Length 1201;
 Best Local Similarity 94.2%; Pred. No. 9.7e-152;
 Matches 818; Conservative 22; Mismatches 19; Indels 9; Gaps 6;

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QY 692 GCAAGTCTGTTCTTACAGTGGGAGAGCAAGTGGCGCAAGCGGCTTGTCTCA 751
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QY 752 CCGGATATATACGCTTTTGGACACAGACAAATGCTTCTTACCGGAGACATGA 811
DB 357 CCGGATATATACGCTTTTGGACACAGACAAATGCTTCTTACCGGAGACATGA 416
QY 812 CCTTGGCGGCACTCTTCTGAGGCACTGATCCAAAGTGGGCGGCTTCTGAGG 871
DB 417 CCTTGGCGGCACTCTTCTGAGGCACTGATCCAAAGTGGGCGGCTTCTGAGG 476
QY 872 TTGAGCAAGTATATGTCGCAAGTGTGATCTGAGATGAGCGGTACCACTATTG 931
DB 477 TTGAGCAAGTATATGTCGCAAGTGTGATCTGAGATGAGCGGTACCACTATTG 536
QY 932 TGGGGGTGTGCTTCTTGTGCTCCGCTTCAAGCGGCGCTCCGCGGCGGTGCCA 991
DB 537 TGGGGGTGTGCTTCTTGTGCTCCGCTTCAAGCGGCGCTCCGCGGCGGTGCCA 596
QY 992 TGTCTTGACATCTTCCCATGATGATGCTCTTCTGAGTATGCTCTGAGCTTGAAG 1051
DB 597 TGTCTTGACATCTTCCCATGATGATGCTCTTCTGAGTATGCTCTGAGCTTGAAG 656
QY 1052 ACTGAAGCTGCTCCACAGCGGATCCGACAGTGTGGCGTGGGCTCCATGCCAACA 1111

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Db	657	ACTAAGCTGCTCCACAGGGCATCGACGCTGGCGTGGGCTCCATGGCAACG	716
Qy	1112	CCTGCTCCTCTTTGACCCCTGCTTCTACCGAGACTGTGCTGNGCACCCTTCTAAC	1171
Db	717	CCTGCTCCTCTTTGACCCCTGCTTCTACCGAGACTGTGCTGNGCACCCTTCTAAC	776
Qy	1172	TTATGAGATGCTGCTCATGTTGGGATGGCGCTGACACGACCACTCACCTGGGCATCA	1231
Db	777	TTATGAGATGCTGCTCATGTTGGGATGGCGCTGACACGACCACTCACCTGGGCATCA	836
Qy	1232	GACACAGATCTACTGAGTCAGCATCAGGGTCCCGACCTCTGGGCTCCTGTTTCCAGAG	1291
Db	837	GACACAGATCTACTGAGTCAGCATCAGGGTCCCGACCTCTGGGCTCCTGTTTCCAGAG	896
Qy	1292	AAGGGGCGACACCTTCTCTCCAGGAGCTGAGACTTTGNGTCTGAGCATMAGGAGTG	1351
Db	897	AAGGGGCGACACCTTCTCTCCAGGAGCTGAGACTTTGNGTCTGAGCATMAGGAGTG	956
Qy	1352	CCAGGMAAGTTTGAAG--TTTGATGATGATGATATTTTGGCTGGGAACTCTACACATCC	1410
Db	957	CMAGGMAAGTTTGAAGTTTGAAGATGAAATATTCGGCTGGGAACTCTACACATCC	1016
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RESULT 11
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DEFINITION     AGENCOURT_14496605 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:69711716 5', mRNA sequence.
ACCESSION      CD559737
VERSION        CD559737.2  GI:36453567
KEYWORDS
SOURCE
ORGANISM       Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 808)
AUTHORS        NIH-MGC http://mgc.ncl.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        On Jun 10, 2003 this sequence version replaced gi:31585805.
                Contact: Daniela S. Gerhard, Ph.D.
                Office of Cancer Genomics
                National Cancer Institute / NIH
                Bldg. 31 Rm10A07 Bethesda, MD 20892
                Email: cgapbs-rt@mail.nih.gov
                Tissue Procurement: Narayan Bhat
                cDNA Library Preparation: Bhat Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNL at:
                http://image.llnl.gov
                plate: irbkl row: c column: 03
                High quality sequence start: 6
                High quality sequence stop: 707.
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/clone="IMAGE:6971716"
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/notes="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK_prev.dat
a Note: this is a NIH_MGC Library."

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Query Match	31.8%;	Score 701.8;	DB 14;	Length 808;
Best Local Similarity	98.8%;	Pred. No. 3.9e-141;		
Matches 728;	Conservative 0;	Mismatches 6;	Indels 3;	Gaps 2;
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Db	748	GAGGCACAGACTCACGAGACATCTCTCAGT-GGACTTCCACGACTCCTTTTCACACTTC	690	
OY	684	AACGTCAAAGCAGTCTGTTCTTTCACAGTGGCAGGAGACAAGATCGGCCAACGCCAGCTTC	743	
Db	689	ACGCTCAAGCAGGTCCTGTTCTTTCACAGTGGCAGGAGACAAGATCGGCCAACGCCAGCTTC	630	
OY	744	GTGCTCAACGGGATGATGACGTCTTTGACACACAGACAACATGTCCTTTACCTGACG	803	
Db	629	GTGCTCAACGGGATGATGACGTCTTTGACACACAGACAACATGTCCTTTACCTGACG	570	
OY	804	GACCATGACCTCGGCGCCACACTCTTGTGTGGGGCACTGATCCAAAACGTGGGCCCATC	863	
Db	569	GACCATGACCTCGGCGCCACACTCTTGTGTGGGGCACTGATCCAAAACGTGGGCCCATC	510	
OY	864	CGGGCTTTTTGGACAAAGTAATAATGTGCACAGAGGTGGTAATCCAGAAATGACGGTAACCA	923	
Db	509	CGGGCTTTTTGGACAAAGTAATAATGTGCACAGAGGTGGTAATCCAGAAATGACGGTAACCA	450	
OY	924	CCTAATTGTGGGGGTGTGGCTTCTTGTCTGTCCCGCTTCACAGGCGCGCTGECCTTGCGCGGT	983	
Db	449	CCTAATTGTGGGGGTGTGGCTTCTTGTCTGTCCCGCTTCACAGGCGCGCTGECCTTGCGCGGT	390	
OY	984	GCTGCCCAATGCTTTGGACATCTTCCCATTGGAATGATATGTCCTTCGAGGGATATGTGCTGGAG	1043	
Db	389	GCTGCCCAATGCTTTGGACATCTTCCCATTGGAATGATATGTCCTTCGAGGGATATGTGCTGGAG	330	
OY	1044	CTTAGAGGGAATGAAAGCTGCTCCACAGACGGGATCCGCAAGTCTGGCGTGGCGGACTCCA	1103	
Db	329	CTTAGAGGGAATGAAAGCTGCTCCACAGACGGGATCCGCAAGTCTGGCGTGGCGGACTCCA	270	
OY	1104	TGCGAACACTGTCTCTCTTTGACCCCTGCTTCTAACCGAGACTGTGCTGTGTGACACGCG	1163	
Db	269	TGCGAACACTGTCTCTCTTTGACCCCTGCTTCTAACCGAGACTGTGCTGTGTGACACGCG	210	
OY	1164	TTTCCATCCTTATGATATGCTGCTCATATGGGATGCGGCGMAACAGGCCAACCTCAACCTGCG	1223	
Db	209	TTTCCATCCTTATGATATGCTGCTCATATGGGATGCGGCGMAACAGGCCAACCTCAACCTGCG	150	
OY	1224	GGCAATCAGACAGATCTACTGATGACATCAAGGAGTCCCGCAGCTTCTTGAGGCTCTGTT	1283	
Db	149	GGCAATCAGACAGATCTACTGATGACATCAAGGAGTCCCGCAGCTTCTTGAGGCTCTGTT	90	
OY	1284	TCCAGAGGAAGGGCGACACTTCTCTCCAGGAAGCTGAGA CTTTGTGTGTAGACATA	1343	

Db 89 TCACATAGGAAGGGCGACACCTTCTCCAGGAGCTGAGACCTT--TTGTTGAGACATA 32
OY 1344 AGGAGTGCCAGGAG 1360
Db 31 AGGAGTGCCAGGAG 15

RESULT 12
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DEFINITION clone CS0D1060YF21 3-PRIME, mRNA sequence.
ACCESSION AL551994 GI:31273810
VERSION AL551994
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12890467.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9600.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1060CC1NP1&cluster=9600.f. Contact :
Feng Jiang Email : fjiang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0D1060CC1NP1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (drr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 31.5%; Score 694.2; DB 9; Length 1201;
Best Local Similarity 92.7%; Pred. No. 2,2e-139;
Matches 788; Conservative 22; Mismatches 31; Indels 9; Gaps 8;

OY 1334 AGGAGAGTTGAGTTGATGATGAATATTTGCTGGCGAACTCTACACATCTTC 1413
Db 1054 AAKKATKCCAKAAKATRRGTTKATRAKMAAATTTGCTGSGACTCTACACATCC-TC 996
OY 1414 AAAACCCACCTGTCTGTCCAGATCTTCCCTGAGTGGCTGAGGAACTCCAAAT 1473
Db 995 AAAACCCACCTGTCTGTCCAGATCTTCCCTGAGTGGCTGAGG-ACCTCCAAAT 939
OY 1474 ATGCATCTTTTGTGTGCTGCTATATGAGAGTGCCTGCTAGAGTTCCAACTGTG 1533
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OY 1534 GATGATCCGTCCTGCTTGAAGTCAAAAGTCTTAATCTTCCCTGCTCACTACACAGAG 1593
Db 881 GATGATCCGTCCTGCTTGAAGTCAAAAGTCTTAATCTTCCCTGCTCACTACACAGAG 822
OY 1594 GGATGCTAAGACAGACCTGACAGTGTATATGCAATATAGCTCGCTGCACTTCCA 1653
Db 821 GGATGCTAAGACAGACCTGACAGTGTATATGCAATATAGCTCGCTGCACTTCCA 762

OY 1654 GCCCAGCCAGAAACTCTGTGTCCACATAGAGCTGAGTGAGAAATATCTTACGCCAG 1713
Db 761 GCCCAGCCAGAAACTCTGTGTCCACATAGAGCTGAGTGAGAAATATCTTACGCCAG 702
OY 1714 GAGAGAGGGGTCTTGATCTTAACCTTTCTGTGGTCTTCAGACAACTCAGAAAGTT-GGGG 1772
Db 701 GAGAGAGGGGTCTTGATCTTAACCTTTCTGTGGTCTTCAGACAACTCAGAAAGTTGGGG 642
OY 1773 GGATCCGAGAGAGTGTGAGTAATAGACCGGCCCTCTTCTGTGGATCAATATGCTG 1832
Db 641 GGATCCGAGAGAGTGTGAGTAATAGACCGGCCCTCTTCTGTGGATCAATATGCTG 582
OY 1833 TAATGTGAGAGTGTGAGCAAGAGAGGAGCAAGTGT-CTTGAAGTTGTGAGAGCTC 1891
Db 581 TAATGTGAGAGTGTGAGCAAGAGAGGAGCAAGTGTCTTTGAAGTTGTGAGAGCTC 522
OY 1892 AGAGTTTCTGGAGTCTTCATTAGAGACCCCATCTGTGTTCCTCCAGAAATTCAGAGAA 1951
Db 521 AGAGTTTCTGGAGTCTTCATTAGAGACCCCATCTGTGTTCCTCCAGAAATTCAGAGAA 462
OY 1952 CAGCACTGGGGCTGGAAATGATCTTTAATGGGCCCAAGGCCAAGCATATGCTCACTA 2011
Db 461 CAGCACTGGGGCTGGAAATGATCTTTAATGGGCCCAAGGCCAAGCATATGCTCACTA 402
OY 2012 CTGCTCGAGAGAGGAGAGATTTCAGAGTCTTCAGAGCTCTCCACAGCTATATTTTA 2071
Db 401 CTGCTCGAGAGAGGAGAGATTTCAGAGTCTTCAGAGCTCTCCACAGCTATATTTTA 342
OY 2072 CAGATTACGGGGGAGACCGGGGTAGACCAAGTGAACCCCTGAGACCCCAAGCTTCAGAGCTCA 2131
Db 341 CAGATTACGGGGGAGACCGGGGTAGACCAAGTGAACCCCTGAGACCCCAAGCTTCAGAGCTCA 282
OY 2132 GTGTCTGCAATCAAGCTTTCAGAGCAAGTGTGATGGGAGCCCTGGGGAATATTAAT 2191
Db 281 GTGTCTGCAATCAAGCTTTCAGAGCAAGTGTGATGGGAGCCCTGGGGAATATTAAT 222
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RESULT 13
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LOCUS BM682980
DEFINITION UT-E-B01-ajd-e-01-0-UI s1 UT-E-B01 Homo sapiens cDNA clone
UT-E-B01-ajd-e-01-0-UI 3', mRNA sequence.
ACCESSION BM682980
VERSION BM682980.1 GI:18992876
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 720)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE 97044477
PUBMED 8889548
CONTACT: Soares, MB
Coordinated laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel.: 319 335 8250
Fax: 319 335 8250
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research

Genetice (www.reagen.com).
Seq primer: M13 Forward
POLY-A=yes.

FEATURES

source

Location/Qualifiers
1..720
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/db_xref="taxon:9606"
/clone="UI-E-EO1-ajd-e-01-0-UI"
/issue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EO1"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=human fetal eye
TAG_LIB=UI-E-EO1
TAG_SEQ=CCGTATACC"

ORIGIN

Query Match 31.4%; Score 691.4; DB 12; Length 720;
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Matches 703; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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720 CTAATGGCGAAGTGCCTGTCTAGAGTTCCAACTGTGATGATCCGCTTGGTGAAT 661
1556 CAAAGTCTTACTCCCTGCTCTCACTCACTCAGACAGGAGATGCTAAGCAGTCACTTC 1615
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660 CAAAGTCTTACTCCCTGCTCTCACTCACTCAGACAGGAGATGCTAAGCAGTCACTTC 601
1616 AGTGGTTTAATGCGAAGATAGCTCCGCTCTGCAAGTTCCAGGCCAGCCAGAACTCCTGTCT 1675
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1676 CCACATAGAGCTGAGCTGAGAAATATCTTTCAAGCCAGAGAGAGGGCTCTGATTTTAA 1735
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1736 CCCTTCCGGGCTCAGACAATCAAGAGTTGGGGGGATACAGAGAGTGGTGGAAAT 1795
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1975 TTAATGGGCCAAGGCCAAGGCATATGCTCTCACTACTGCTGAGAAAGGAGAGATTC 2034
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QY 2035 AGGTCTCCAGAGAGCTCTCCCTGACCCAGATATGTTTACAGATTAAGGGGGACCGGGTGA 2094
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DB 180 AGGTCTCCAGAGAGCTCTCCCTGACCCAGATATGTTTACAGATTAAGGGGGACCGGGTGA 121
QY 2095 GCCAGTGAACCCCTGAGAGCCCGCAGCTTCAAGGCTCAGTGTCTGCAAGTCAAGCTTCACA 2154
120 GCCAGTGAACCCCTGAGAGCCCGCAGCTTCAAGGCTCAGTGTCTGCAAGTCAAGCTTCACA 61
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60 GGCATTGTGATGGGCGCAGCTTGGGGAAATATTAATTTGTGAGA 15
RESULT 14
BM718996
LOCUS
DEFINITION
UI-E-EO1-ajd-e-01-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-ajd-e-01-0-UI 5', mRNA sequence.
ACCESSION
BM718996
VERSION
BM718996.1 GI:19037463
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 680)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com).
Seq primer: M13 Reverse.
FEATURES
source
1..680
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EO1-ajd-e-01-0-UI"
/issue_type="fetal eye"
/dev_stage="fetal"
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/clone_lib="UI-E-EO1"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

Qy 498 GAGCTGCTGGGCGGCACTGGGGCCGCGAGCGGTAACGGGTTTGACAGTGGCGCTC 557
Db 501 GAGCTGCTGGGCGGCACTGGGGCCGCGAGCGGTAACGGGTTTGACAGTGGCGCTC 560
Qy 558 CTCTTCTGGTGGGCAAGCTTCCAAACCGCAAGGCGCCGCAAGGTCAACCGGCTGCTG 617
Db 561 CTCTTCTGGTGGGCAAGCTTCCAAACCGCAAGGCGCCGCAAGGTCAACCGGCTGCTG 620
Qy 618 GAGCTGAGGCGACAGACTCAAGGAGATCTCTGAGTGGGACTTCCACGACTCTTCTTC 677
Db 621 GAGCTGAGGCGACAGACTCAAGGAGATCTCTGAGTGGGACTTCCACGACTCTTCTTC 680
Qy 678 AACCTCAGCGCTCAAGGAGTCTGTCTTACAGTGGCGAGGACAAG 724
Db 681 -ACCTCAGCGCTCAAGGAGTCTGTCTTACAGTGGCGAGGACAAG 726

Search completed: June 14, 2004, 16:22:35
Job time : 5678 secs

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